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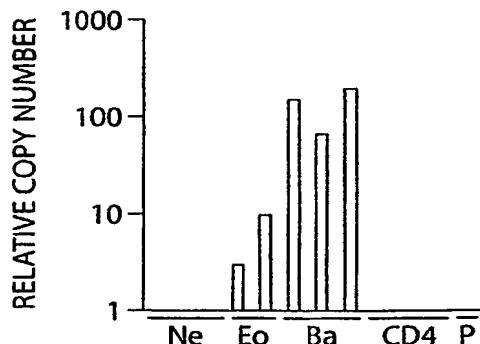


Fig. 1A

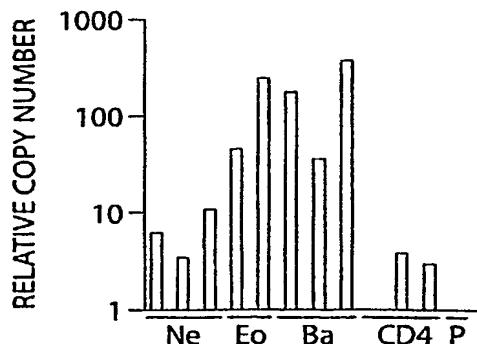


Fig. 1B

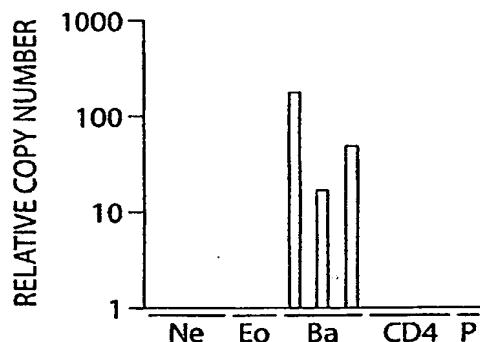


Fig. 1C

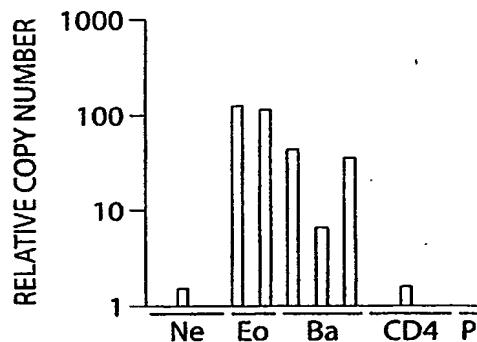


Fig. 1D

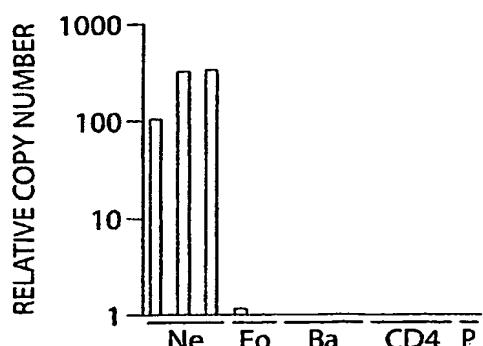


Fig. 1E

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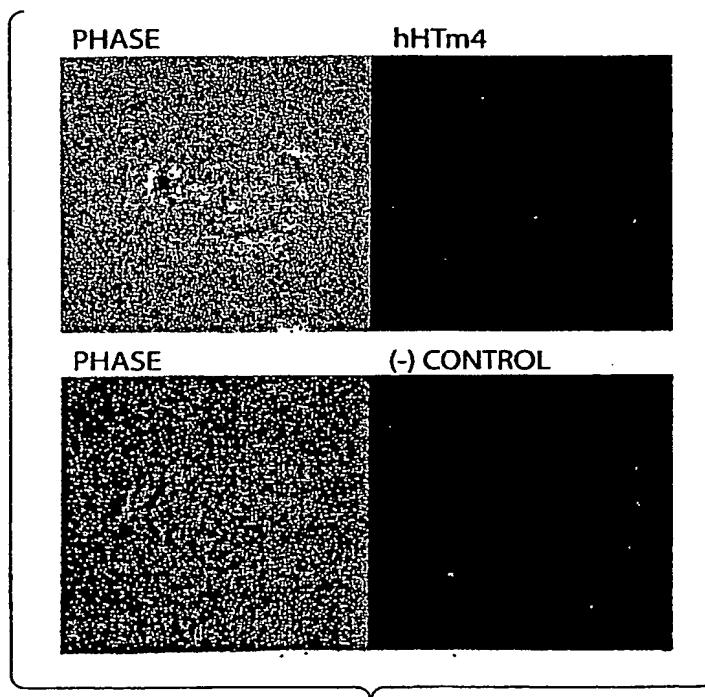


Fig. 2

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Figure 3. Granulocyte subtype-specific transcripts for ion channels and receptors

<i>Ion Channels Transcript (Accession #, GenBank)</i>	<i>Cell-type^a Ba, Eo Ne</i>	<i>MC 0.1 0.7</i>	<i>Ba 0.1 0.4</i>	<i>Ne 1.7 0.4</i>	<i>Pi 0.4 13/4</i>	<i>CD4 0.0 0.9</i>	<i>CD8 0.1 0.9</i>	<i>CD14 0.0 0.1</i>	<i>CD19 0.0 8/6</i>	<i>Fb 0.3 0.1</i>	<i>Tc^b</i>	<i>Gene Functions</i>
<u>Ca²⁺ channel type A1 D (BE550599) aquaporin 9 (NM_020980) 60294</u>											0.0 0.2	7
K ⁺ channel Kir 1.3 (U73191) 600359	Ne	0.9	0.2	0.4	99.5	0.7	0.2	0.0	0.8	0.0	0.0 0.0	5
K ⁺ channel Kir 2.1 (AF153820) 600681	Ne	0.7	3.8	5.3	40.7	0.4	0.2	0.5	1.5	0.7	1.1 1.1	6
<u>GPCR histamine H₄ R (AF312230) 606792</u>	Ba	0.7	34.2	9.4	0.7	0.4	0.8	0.5	0.6	0.0	0.1 0.1	0
<u>PGE² R type 3a2 (X83858) 176806 C3a R (U62027) 605246 CCR3 (NM_001837) 601268</u>	Ba, Eo Ba, Eo Ba, Eo	0.8 11.8 0.6	10.3 55.7 117.4	0.1 39.4 90.9	0.7 2.0 24.9	0.6 1.6 0.2	0.3 1.5 0.5	0.2 0.4 0.4	0.2 0.3 0.2	0.5 0.6 0.2	1.7 0.5 0.4	0 0 0
<u>CRTH2 (NM_004778) 604837</u>	Ba, Eo	1.1	26.0	38.2	2.0	0.8	1.4	1.0	1.2	0.9	0.5	0
<u>EMR-1 (NM_001974) 600493</u>	Ba, Eo	0.8	33.5	90.9	4.2	3.4	1.7	0.8	7.1	1.6	0.5	1
<u>adenosine A₃ R (NM_000677) 600445 P2Y2 purinergic R (NM_002564) 600044</u>	Eo Eo	2.6 0.1	2.9 0.1	15.4 5.5	2.3 0.1	1.2 0.2	1.6 0.1	0.5 0.3	2.0 1.2	0.5 0.2	0.5 0.1	0
GPR 105 purinergic R (NM_014879)	Eo	2.6	2.9	15.4	2.3	1.2	1.6	0.5	2.0	0.5	0.5 0.5	2
<u>GPR, Edg-4 (AF011466) 605110</u>	Eo, Ne Eo, Ne	1.3	2.8	15.9	24.2	0.1	3.6	5.0	3.8	1.9	0.9	2
<u>pARI-like GPR43 (NM_005306)</u>												

facilitates uptake of the metalloids arsenite and antimonite
Andersen syndrome (170390)
and Bartter syndrome (241200)
Andersen syndrome (170390)
and Bartter syndrome (241200)

expression of HRH4 conferred sensitivity
signaling pathways
anaphylatoxin receptor
importance for eosinophil responses

mediate signals to the interior of the cell via activation of heterotrimeric G proteins
Probably involved in cellular response to a hormone
cardioprotective function
P2RY2 may participate in control of the cell cycle of endometrial carcinoma cells
GPR105 is a G-protein-coupled receptor identifying a quiescent, primitive population of hematopoietic cells restricted to bone marrow; GPR105 might play an important role in peripheral and neuroimmune function

edg-4 mRNA was expressed in mouse islets; edg-4 (loa2) r is a distinctive functional marker for ovarian carcinoma, and is expressed both as the wild-type and a carboxy-terminal extended gain-of-function mutant.
the highest levels of qpr43 were

Fig. 3A

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<u>603823</u>	<u>C5a R (NM_001736) 113995</u>	Ne	2.3	21.6	13.6	92.6	2.3	1.2	0.5	25.6	1.0	0.4	5	found in immune cells; gpr43 is highly restricted in hematopoietic tissues receptor for the chemotactic and inflammatory peptide anaphylatoxin C5a; this receptor stimulates chemotaxis, granule enzyme release and superoxide anion production.
<u>CXCR1 IL-8R (NM_000634) 146929</u>		Ne	0.2	4.3	0.3	83.4	0.4	0.3	0.2	0.2	0.1	0.1	0	receptor to interleukin-8, which is a powerful neutrophils chemotactic factor. binding of il-8 to the receptor causes activation of neutrophils. this response is mediated via a g-protein that activate a phosphatidylinositol-calcium second messenger system. this receptor binds to il-8 with a high affinity and to mgsa (gro) with a low affinity.
<u>CXCR2 IL-8R (NM_001557)</u>		Ne	0.2	1.1	1.5	112.1	2.7	0.3	0.8	0.7	0.6	0.0	1	receptor to interleukin-8, which is a powerful neutrophils chemotactic factor. binding of il-8 to the receptor causes activation of neutrophils. this response is mediated via a g-protein that activate a phosphatidylinositol-calcium second messenger system. this receptor binds to il-8 with a high affinity and to gro/mgsa and nap-2 also with a high affinity.
<u>formyl peptide R 1 (NM_002029) 136537</u>		Ne	2.8	23.5	8.8	282.9	3.6	1.3	0.7	62.6	1.1	0.5	0	HIGH AFFINITY RECEPTOR FOR N-FORMYL-METHIONYL PEPTIDES, WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF FML TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED

Fig. 3B

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Fig. 3C

VIA A G-PROTEIN THAT ACTIVATES PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. likely FPR2, mediates superoxide production at high concentrations of MIF.									
formyl peptide R 2 (<u>U81501</u>)	Ne	0.4	0.5	0.6	75.5	0.1	1.0	0.6	6.0
GRPR77 (<u>NM_018485</u>)	Ne	0.1	0.9	0.8	3.4	0.0	0.3	0.2	1.0
GRPR86 purinergic R (<u>NM_023914</u>)	Ne	0.3	0.2	17.9	88.2	1.9	0.1	0.2	12.3
PAR2 (<u>BE2965369</u>) <u>600933</u>	Ne	0.1	0.3	2.2	36.2	0.1	0.7	0.1	1.6
<u>Other Receptors</u>									
Fc ε RI α (<u>BC005912</u>) <u>147138</u>	Ba	19.4	219.0	4.6	5.5	1.4	5.1	0.8	1.4
HITm4 (<u>L35848</u>) <u>606498</u>	Ba	0.6	133.1	6.9	3.5	0.2	0.5	0.4	0.1
IL-3 R (<u>NM_002183</u>) <u>308385</u>	Ba	0.6	52.6	2.0	0.7	0.2	0.3	0.2	0.7
CD244 NK cell R <u>NM_016382</u> <u>605554</u>	Ba, Eo	0.3	56.0	16.5	1.2	0.1	0.4	3.5	5.2
fibroblast growth factor R 2 (<u>NM_022969</u>) <u>176943</u> [<u>FGF-R α (M75914)</u>] <u>1477851</u>	Ba, Eo	0.1	27.9	12.1	0.2	0.1	0.1	0.2	0.1
Siglec 8 (<u>NM_014442</u>) <u>605639</u>	Eo	1.8	0.3	17.4	0.4	0.3	0.2	0.1	0.2
CD117 c-KIT (<u>NM_000222</u>) <u>164920</u>	MC	89.0	7.2	4.2	1.2	0.8	0.2	0.5	0.1
SiglecB D86358 604405	MC	5.6	0.2	0.0	0.2	0.5	0.0	0.0	0.4
Fc ε RIβ (<u>NM_000139</u>) <u>147138</u> low density lipoprotein R	MC, Ba	22.3	44.3	0.4	0.6	1.6	0.5	0.2	0.0
	MC, Ba	20.7	20.4	1.3	1.8	2.3	2.1	3.4	0.8
									0.3
									0.1
									6.3
									34

Fig. 3D

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isoforms 2 to 6 block apoptosis (in vitro), does not induce apoptosis.									
<u>decoy R1, TRAILR3 (AF012536)</u>	Ne	0.1	1.5	7.7	78.7	0.5	0.2	0.1	0.7
<u>FCyR IIc2 (U90939)</u>	Ne	1.5	2.4	7.8	59.9	0.3	0.2	0.1	7.2
<u>FCyR IIc3 (U90940)</u>	Ne	2.4	10.7	10.0	84.3	3.0	1.4	0.6	14.0
<u>FCyR III (J04162) 146740</u>	Ne	0.7	1.6	1.9	199.6	6.6	1.3	1.3	2.2
<u>G-CSF R (NM_000760) 138971</u>	Ne	0.1	0.4	1.6	163.6	0.2	0.8	0.2	25.5
<u>IL-13 R (U81379) 308385</u>	Ne	0.3	0.2	2.0	14.1	0.4	0.4	0.3	2.9
<u>IL-1R, type II (NM_004633) 47811</u>	Ne	0.1	0.1	53.5	0.2	0.4	0.1	0.2	0.0
<u>IGFR 1 (NM_000875) 147370</u>	Ne	0.3	3.5	5.0	17.4	1.6	0.1	2.8	2.4
<u>IGFR 2 (NM_000876) 147280</u>	Ne	4.6	0.9	5.4	85.3	1.7	2.9	8.7	8.4
<u>leukocyte immunoglobulin-like R A2 (NM_006866) 604812</u>	Ne	0.5	5.8	4.3	41.2	1.8	0.0	0.1	11.6
<u>Toll-like R 1 (AL050262) 601194</u>	Ne	0.6	0.3	1.2	31.5	1.6	0.8	0.7	3.0
<u>Toll-like R 2 (NM_003264) 603028</u>	Ne	0.9	6.0	1.3	83.8	1.6	1.3	0.1	26.3
<u>Toll-like R 6 (NM_006068)</u>	Ne	0.5	1.0	0.9	8.8	0.1	0.9	0.9	2.1

a. Cell-type specificity was obtained by comparing the "normalized AD" levels of each gene in mast cells (MC; average of 2 experiments), basophils (Ba; average of 3 experiments), eosinophils (Eo; average of 4 experiments), neutrophils (Ne; average of 4 experiments), platelets (Pl), CD4⁺ cells (CD4), CD8⁺ cells (CD8), CD14⁺ cells (CD14), CD19+ cells (CD19) and nasal polyp-derived cultured fibroblasts (Fb).

Fig. 3E

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CB cultured MCs	Basophils	cultured basophils	Eosinophils	Neutrophils	platelets	Erythrocytes	CD4	CD8	CD14	CD19	
Spink5	21	17	11	22	16	30	15	28	36	129	104
chymase human	1221	47	65	45	12	101	62	108	59	104	45
tryptase alpha	21179	212	40	33	25	184	139	104	17	52	39
tryptase beta	25414	195	113	49	28	152	10	122	113	93	6
tryptase delta	349	45	6	23	55	74	113	11	10	42	11
tryptase gamma	654	56	19	38	78	28	24	81	230	142	83
TRPV2	129	37	15	97	99	259	137	133	67	97	110
ANKTM1_	28	28	8	38	30	96	18	14	46	11	28
Cannabinoid receptor type 1	50	41	14	47	36	27	61	41	56	18	54
Cannabinoid receptor type 2	160	369	226	578	177	271	530	324	232	212	421

Fig. 4A

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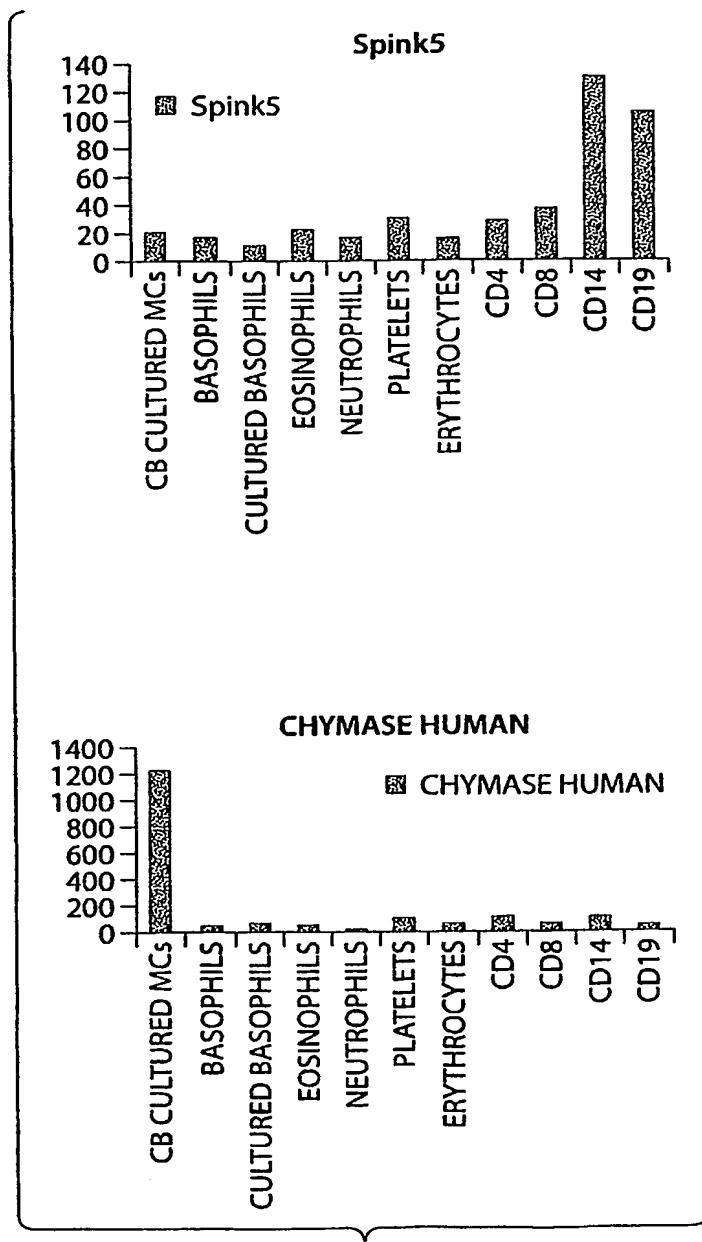


Fig. 4B

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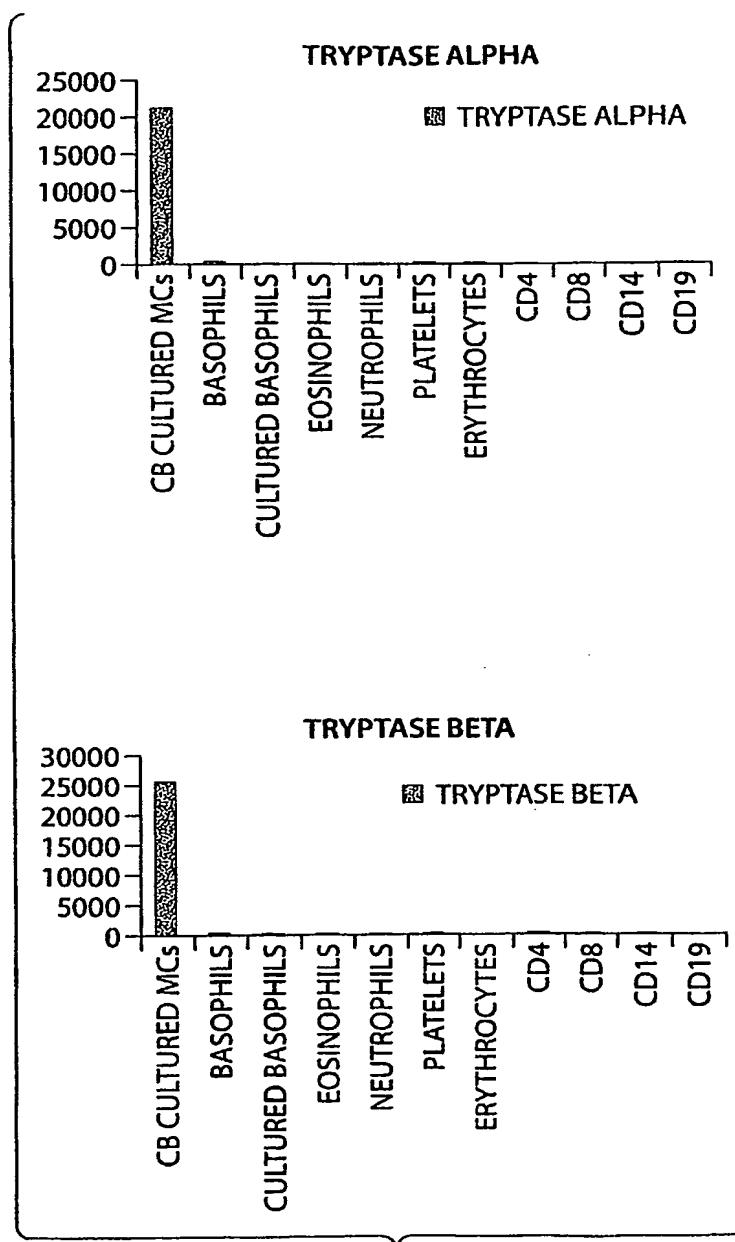


Fig. 4C

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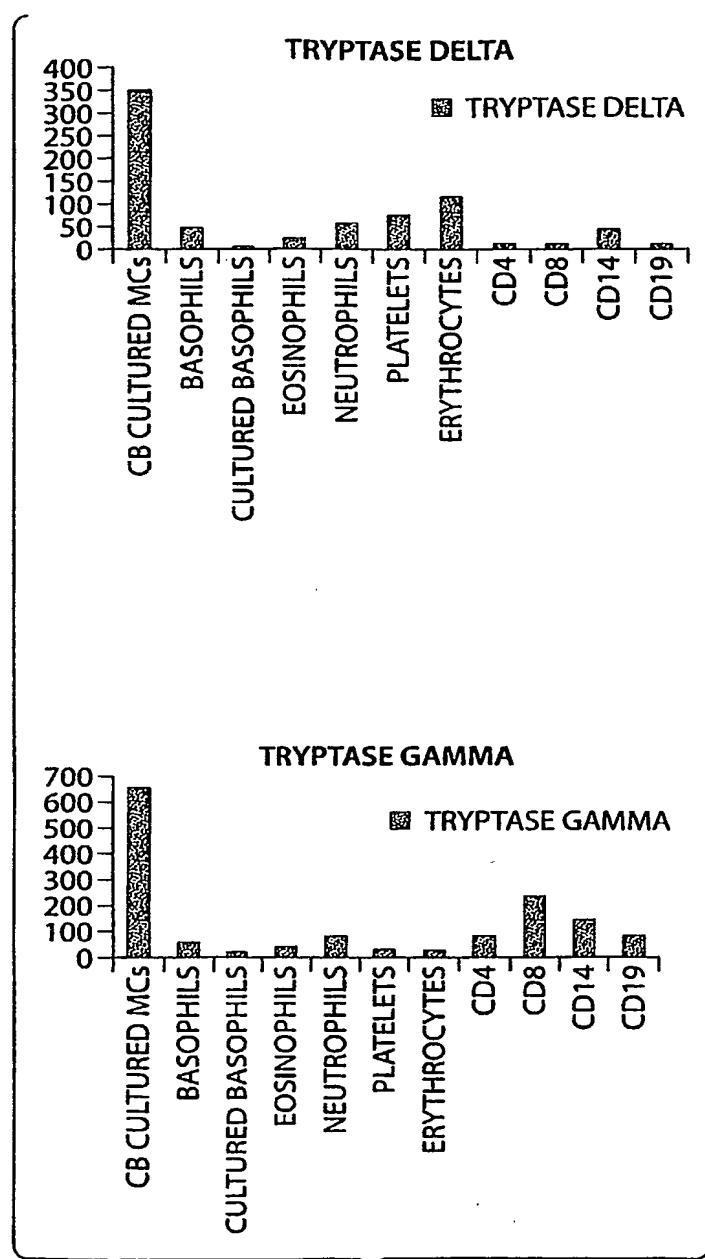


Fig. 4D

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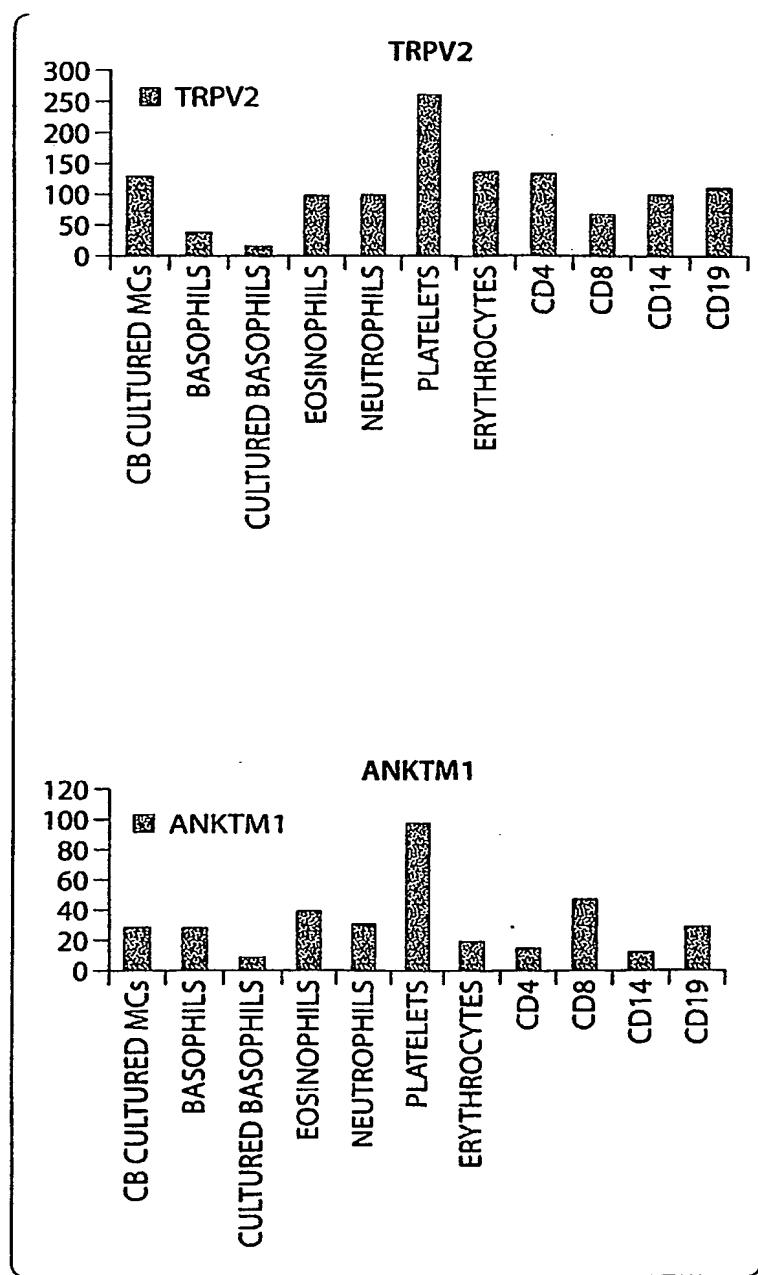


Fig. 4E

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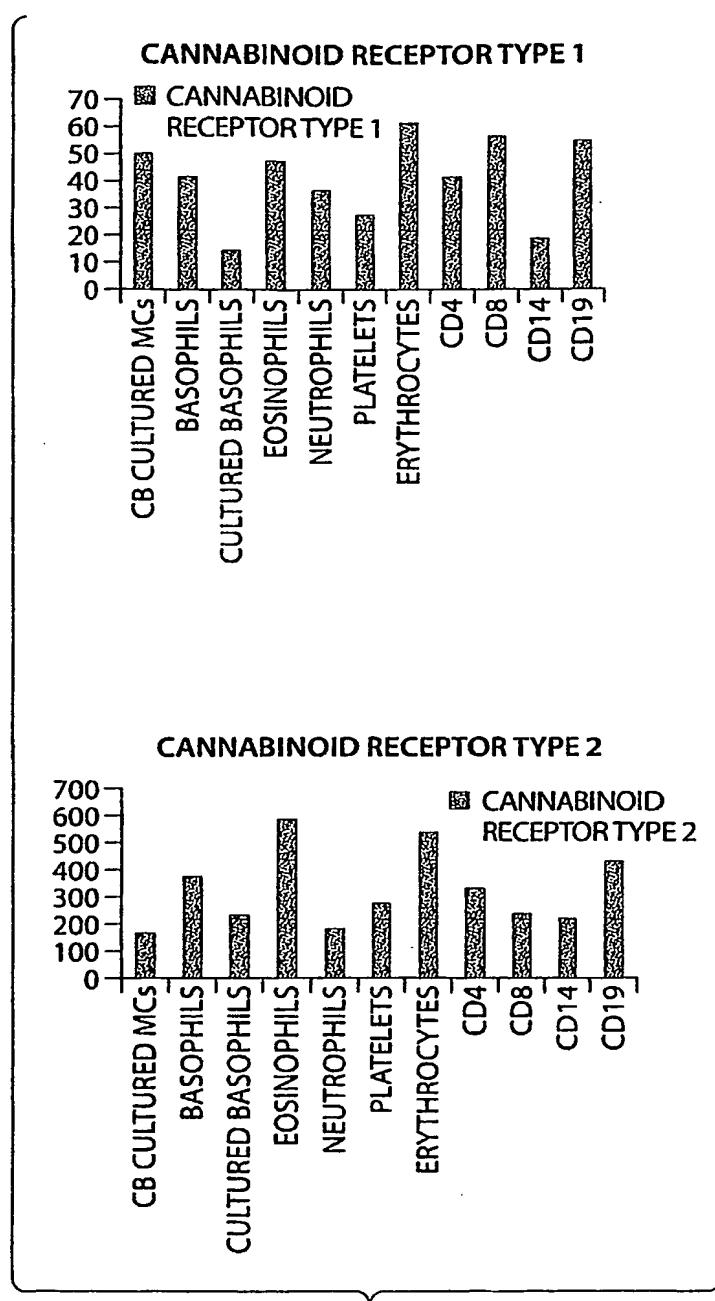


Fig. 4F

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CB cultured MCs	Basophils	cultured basophils	Eosinophils	Neutrophils	platelets	Erythrocytes	CD4	CD8	CD14	CD19
86	28	39	26	37	125	46	103	95	85	28
4	45	1004	59	84	18	68	31	68	451	13
165	84	51	258	1261	31	42	13	18	1105	125
375	780	227	1755	4237	199	375	286	58	2963	214
49	614	384	461	3269	146	318	8	9	1247	52
28	50	45	154	389	120	148	127	35	539	86
7	58	34	18	23	13	106	14	286	68	204
22	17	21	27	28	35	11	28	110	88	111
30	54	134	66	61	149	95	39	247	147	271
35	138	81	88	93	191	132	57	257	21	267
24	31	23	21	21	53	27	33	135	19	173
139	140	85	157	144	280	210	35	239	152	196
11	45	41	50	41	88	15	19	72	77	85
41	43	31	20	52	31	121	96	163	26	193
27	83	24	41	49	61	239	92	323	56	72
68	89	41	51	95	75	97	76	169	36	196
144	621	83	1334	2386	107	146	145	52	2154	99
18	14	5	28	37	86	12	13	14	32	23

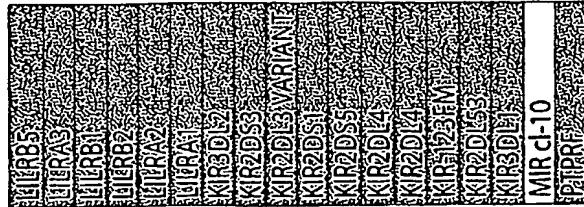


Fig. 5A

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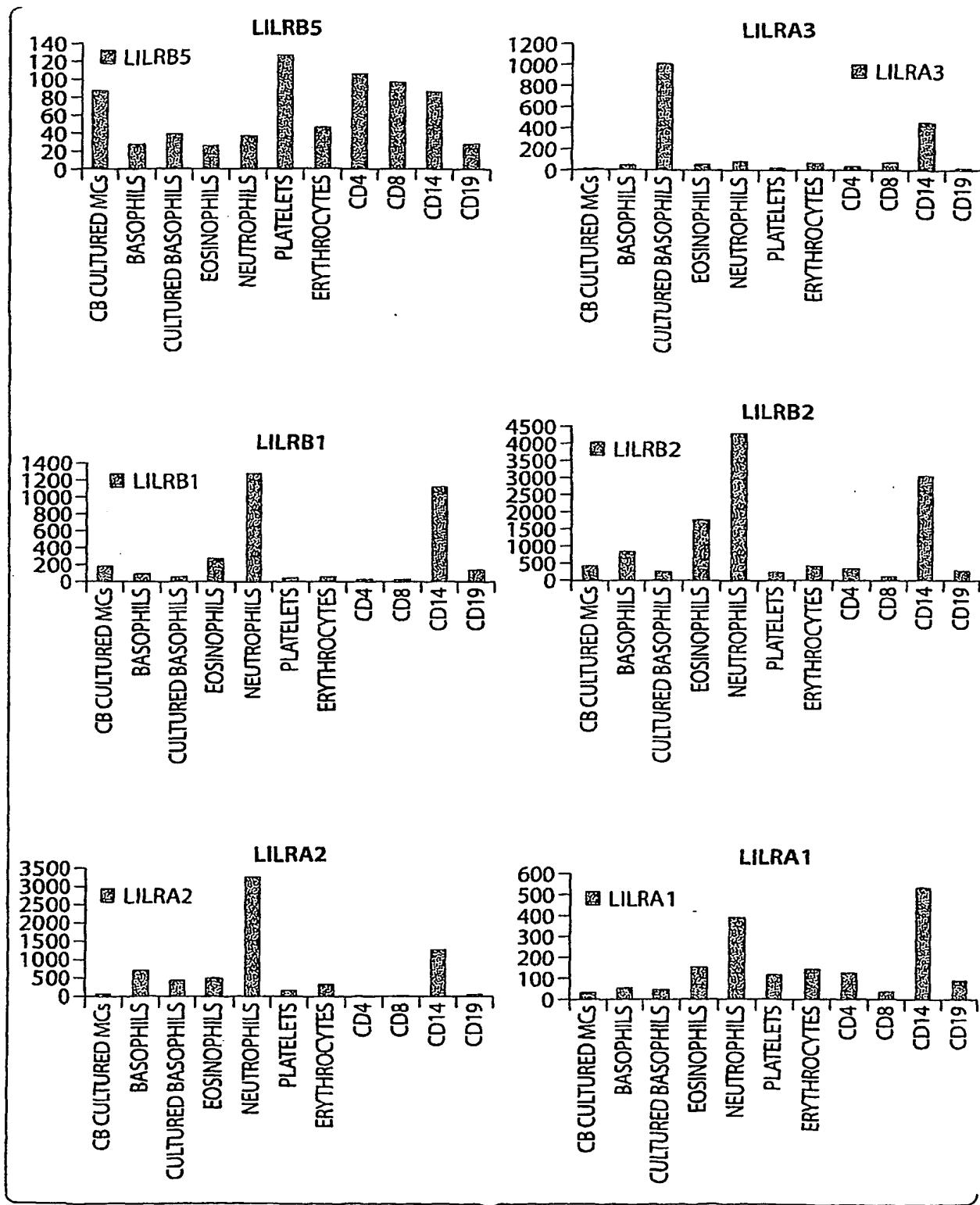


Fig. 5B

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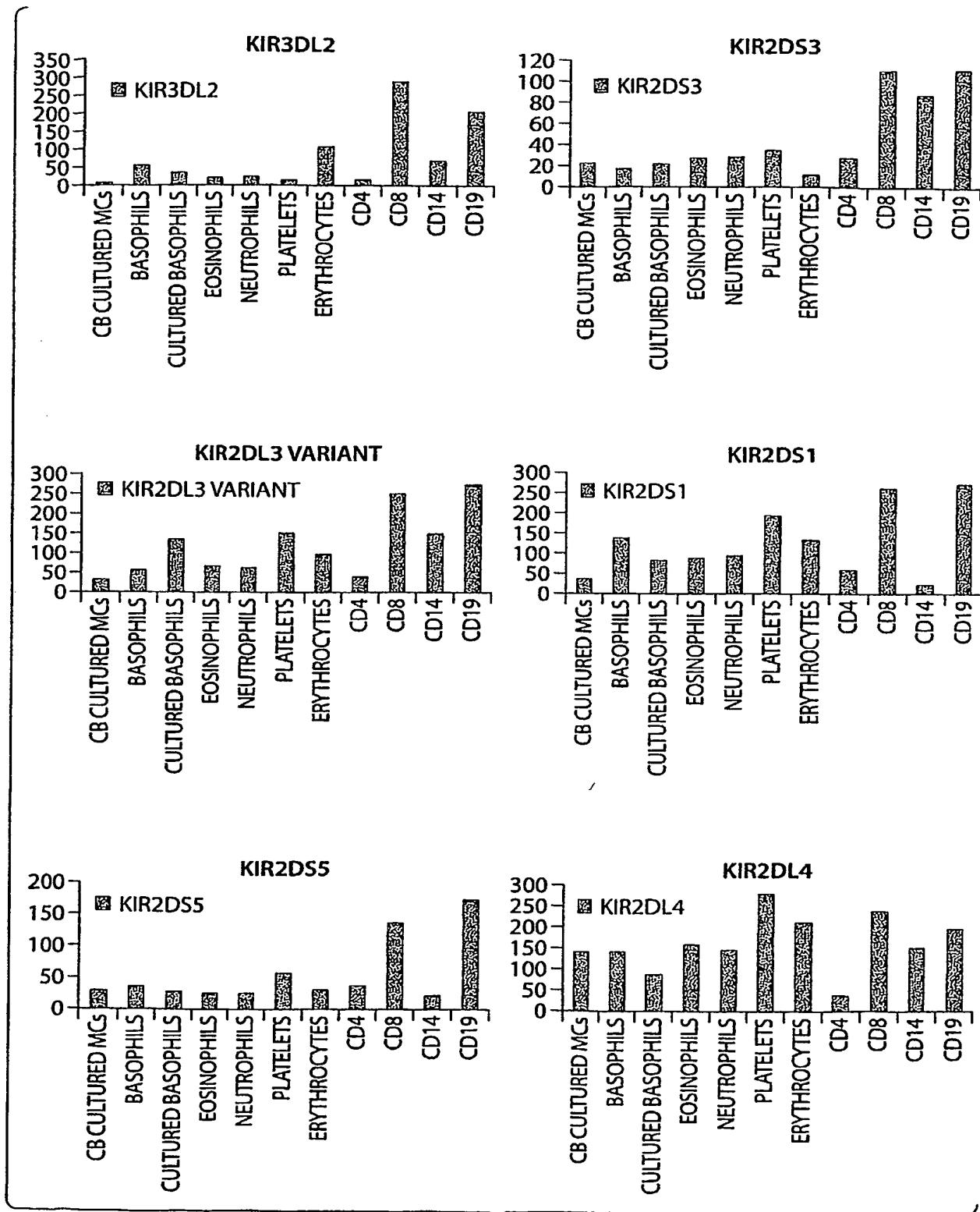


Fig. 5C

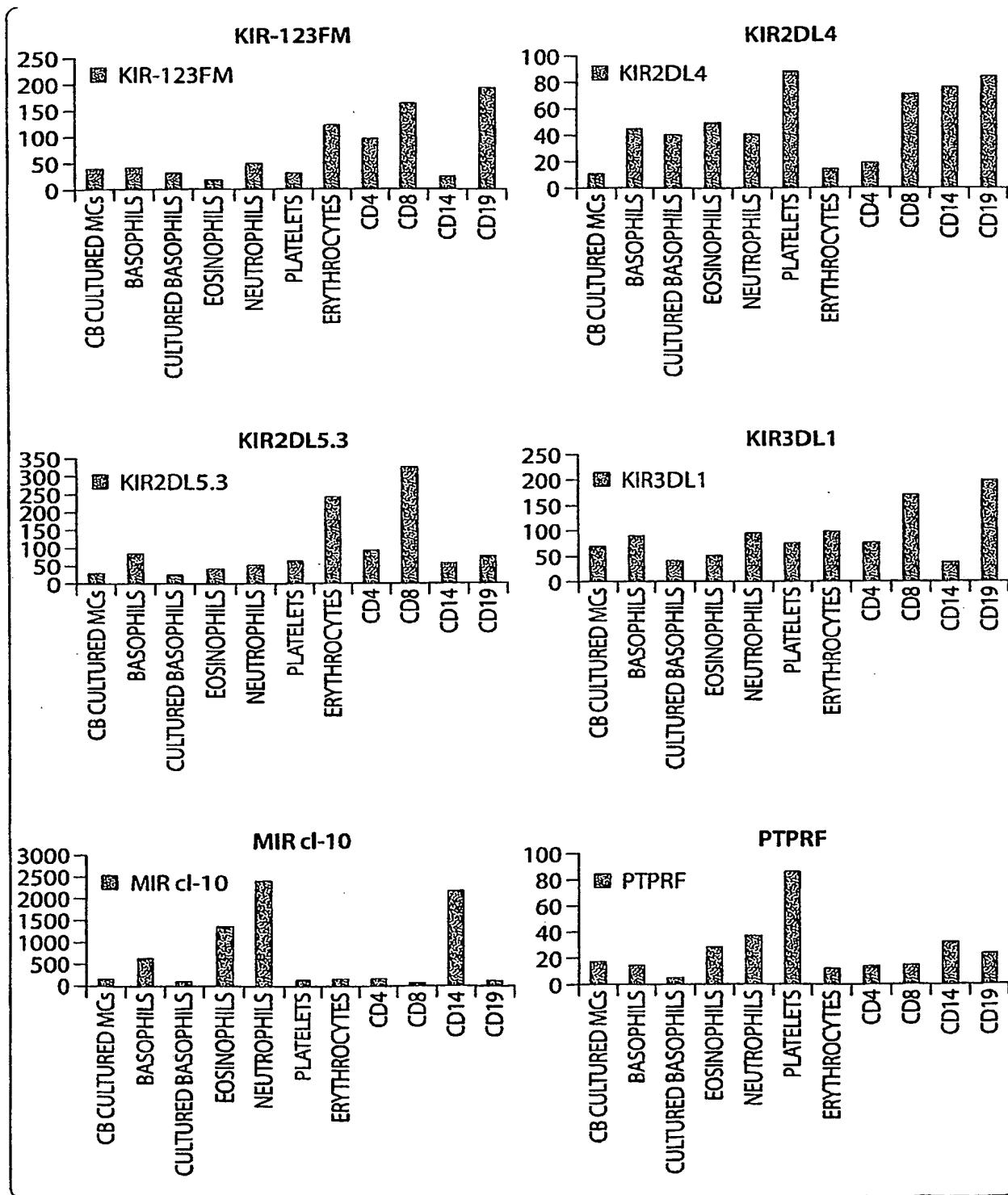


Fig. 5D

Table E1. The complete list of granulocyte subtype-selective transcripts. Selectivity Index (S.I.) was calculated by comparing the "normalized AD" level of a cell type or of two cell types with the maximal gene expression level of the other 8 or 9 cell types including platelets (Pl), CD4⁺ cells, CD8⁺ cells, CD19⁺ cells and nasal polyp-derived cultured fibroblasts (Fb). When the result was accompanied by presence call, it was shown as a bold numeral. Italic numerals show that the raw AD levels were associated with absence call by the GeneChip analysis software. Transcripts having S.I. >3-fold were shown in A-H. Abbreviations used in the table through A-I were (small); the results obtained by the small sample protocol (see materials and methods), R: receptor, and ICN: ion channel.

A. Basophil (Ba)-selective transcripts (1/2).

Probe set	Accession #	Transcripts	MC cord	MC blood	MC lung	Ba 1 (small)	Ba 2 (small)	Ne 1 (small)	Ne 2 (small)	Ne 3 (small)	Ne 4 (small)	Eo 3 1	Eo 3 2	Eo 4 1	Eo 4 2	Ne 4 1	Ne 4 2	Fb Basal					
207539_s_at	NM_000589.1	IL4	0.2	0.7	10.4	16.9	134	0.1	0.3	0.0	0.0	1.2	0.2	0.0	0.0	0.1	0.1	73348					
210254_at	L35848.1	R	Hifm4	0.8	0.4	115.6	130.1	153.6	2.4	1.7	21.8	1.7	0.1	0.9	3.6	9.5	0.2	0.5	3824				
205513_at	NM_001062.1	R	vitamin B12 binding protein	15	12	98.9	149.3	110.9	3.2	2.2	161	19.4	45	63	8.1	1.8	0.7	1.4	0.9	0.7	20322		
206148_at	NM_0002183.1	R	IL-3R	1.0	0.7	6.2	80.2	71.3	1.7	1.7	1.8	29	0.3	0.4	0.2	1.9	0.2	0.3	0.7	0.1	16.62		
214920_at	R33964	R	FLJ11022Ris	0.1	1.1	4.9	13.1	15.4	0.1	0.2	0.7	0.5	1.0	0.4	0.5	0.7	0.1	0.1	0.3	0.1	16.049		
201825_s_at	AL572542	R	CG449	3.3	1.6	21.4	74.9	46.5	21	12	0.1	1.2	0.1	0.1	0.2	0.1	1.3	0.7	1.4	0.8	15.045		
213338_at	AI478147	R	ATPase Class V, type 10D	1.2	2.9	39.9	76.3	118.9	23	1.7	3.7	1.9	2.1	1.4	2.3	6.8	0.7	0.9	2.5	5.0	4.1	14.398	
211734_s_at	BC005912.1	R	Fc epsilon RI alpha	10.5	28.4	210.0	220.8	226.2	84	2.1	4.8	29	0.3	0.7	45	16.6	1.4	5.1	0.8	1.4	0.4	0.2	12.703
213694_at	BF447246	R	KIAA0560	0.1	0.0	3.7	13.0	15.6	0.3	0.4	0.4	0.4	0.9	0.7	0.7	0.6	0.1	0.1	0.2	0.2	0.2	12.272	
206363_at	NM_0055602	R	c-Maf	3.7	1.4	36.5	75.7	66.4	12	0.1	0.2	0.2	0.2	0.1	0.2	10	0.6	4.8	2.7	0.5	1.0	0.0	11.927
203373_at	NM_003877.1	R	SOC52	2.1	3.9	21.7	85.0	112.2	4.6	4.7	9.4	65	0.7	1.2	0.3	2.5	1.6	3.2	3.5	0.8	0.9	3.6	9.8282
207538_at	NM_000589.1	R	IL4	0.3	0.1	5.4	98	92	0.4	0.4	0.0	0.3	0.1	0.0	0.4	0.7	0.8	0.4	0.3	0.1	0.1	0.1	9.8156
213684_s_at	BF671400	R	LIM-protein	0.6	0.1	11.1	21.0	20.6	1.9	1.6	2.4	1.8	0.8	0.6	1.5	2.5	0.1	0.0	0.3	1.0	0.0	0.1	8.9245
209360_s_at	D43958.1	R	AML1b protein	10.4	24	53.2	131.1	90.5	85	7.0	13.8	11.3	0.5	0.5	42	1.3	4.1	5.9	1.3	2.5	3.1	8.7543	
220234_at	NM_0040562	R	carbonic anhydrase VIII	0.4	0.1	11.7	102	60	12	0.1	0.2	0.4	0.8	0.9	0.1	0.5	0.5	1.1	0.1	0.1	0.8	0.0	8.1309
210643_at	AF053712.1	R	osteoprotegerin ligand	0.1	0.3	1.8	34	60	0.7	0.4	0.3	0.2	0.4	0.1	0.3	0.1	0.1	0.1	0.3	0.2	0.2	7.6628	
202911_at	AF132818.1	R	colon knuppel-like factor	0.1	0.0	1.8	102	88	0.3	0.5	1.5	0.8	1.1	0.7	0.8	0.5	0.2	0.2	0.4	0.2	0.1	7.239	
204309_at	NM_000781.1	R	CYP11A	0.3	0.1	2.6	6.1	5.6	0.1	0.3	0.5	0.5	1.0	0.1	0.1	0.9	0.3	0.1	0.0	0.3	0.7	0.7	6.8366
203372_s_at	AB004903.1	R	SOC52	0.6	1.6	9.2	85	15.9	1.4	2.4	0.9	0.2	0.7	0.6	0.4	0.8	0.8	1.3	0.3	0.3	1.4	0.7	6.8271
207463_X_at	NM_002771.1	R	serine protease 3 (trypsin 3) acid sphingomyelinase-like	1.0	1.0	4.8	100	109	0.4	1.0	1.0	1.2	1.2	0.9	1.0	1.8	0.4	0.6	0.3	0.7	1.2	6.7218	

Fig. 6A-1

ProbeSet	Accession #	Transcripts	MC cord blood	MC, lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo	Eo3 (small)	Eo4 (small)	Ne	Ne3 (small)	Ne4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ba5L		
213674_at	AA873600	phosphodiesterase clone DN72943400213	4.7	2.0	20.8	30.6	25.9	21	28	3.8	1.7	0.5	1.1	1.3	0.1	0.2	3.8	0.2	3.2	6.8846		
214873_at	AL137651.1	protein P3	0.1	0.4	3.7	15.5	24.4	20	0.9	2.5	2.3	0.2	0.1	0.6	0.1	1.1	1.5	0.5	0.6	0.7	6.2585	
204928_s_at	NM_0198482	prostate carcinoma tumor antigen (pcba-1)	23	15	9.8	49.0	34.3	3.7	3.3	4.8	42	1.6	1.0	1.9	2.2	4.1	1.8	3.0	0.8	2.0	2.6	6.2142
208935_s_at	L781321	phosphomannomutase 2 (PMM2)	22	12	9.9	19.1	16.6	23	15	3.6	25	1.1	1.1	1.9	0.9	1.8	1.8	2.0	2.0	1.4	0.8	6.2011
203201_at	NM_0003031	CG49	1.8	0.3	10.7	15.9	6.5	0.9	0.6	1.2	0.9	0.8	0.4	1.1	1.3	1.0	1.3	1.2	1.1	1.1	6.1557	
201805_s_at	NM_0160021	CG49	1.8	3.1	11.0	27.5	15.1	16	1.1	1.4	2.1	1.1	1.4	1.3	1.8	1.6	1.1	1.1	1.1	0.6	5.6407	
213421_X_at	AV0007273	serine protease 4 (trypsin 4)	1.8	1.7	5.9	12.5	11.4	10	0.5	1.2	0.5	1.2	1.7	1.2	1.2	0.9	1.0	1.2	1.0	0.4	1.7	5.4082
209348_s_at	AF055376.1	c-Maf, short form	6.4	4.9	29.6	47.7	42.3	0.8	0.3	0.4	0.6	0.3	0.0	0.9	1.4	1.0	1.3	3.1	0.9	0.7	1.4	5.3183
213343_s_at	AL041124	hypothetical protein PP1665	0.9	0.2	12.2	17.0	12.0	35	1.7	0.5	0.6	0.1	0.3	0.8	0.4	0.6	1.5	2.6	0.7	1.6	1.3	5.2721
202491_s_at	NM_0016640	Kappa B-associated protein	1.6	3.8	23.9	51.9	43.5	46	4.0	7.1	7.3	1.6	2.1	2.5	2.3	1.7	3.7	7.4	3.2	4.7	4.2	5.107
221021_s_at	NM_030877.1	Bos taurus t14 protein	6.9	3.2	7.2	29.2	58.9	28	3.2	5.4	6.3	0.9	1.2	1.8	1.6	2.2	2.4	2.0	3.5	1.8	4.9129	
213346_s_at	BE748563	hypothetical protein BC015148	2.7	1.8	17.5	38.8	25.8	40	6.7	6.2	4.8	14	0.9	0.8	1.1	0.2	1.2	1.5	0.6	1.1	1.9	4.8879
208764_at	AL022312	mannose (beta-1,4)-glycoprotein	0.0	0.9	4.1	6.1	5.8	0.8	1.4	0.9	14	0.6	0.1	0.5	0.2	1.0	0.4	0.2	0.2	0.4	4.8555	
207067_s_at	NM_0021121	beta-1,4-N-acetylglucosaminyltransferase	64.1	14.7	1052	164.9	165.7	34	1.4	4.1	28	21	1.2	4.6	14.0	24	0.8	0.9	1.1	0.7	0.2	4.6305
210375_s_at	X33883.1	histidine decarboxylase	1.0	0.6	24	11.5	17.0	0.3	0.1	0.1	0.0	0.4	0.7	0.9	0.7	0.3	0.3	0.2	0.2	0.5	1.7	4.6103
206306_at	NM_001036.1	GPR	2.1	1.1	3.7	11.0	7.8	1.0	0.6	1.5	0.5	1.2	0.3	1.5	0.9	1.1	0.7	0.3	1.0	0.2	0.4	4.5552
210001_s_at	AB03043.1	tyrosine receptor kinase 3 (TKR3)	5.2	0.2	3.0	24.1	29.9	21	3.0	3.2	3.4	0.3	1.0	0.8	1.3	0.8	0.8	0.8	0.0	0.3	0.9	4.5248
		SOC51																				
		serine (or cysteine) proteinase inhibitor, class B (or albumin), member 2 (SERPINB2)	0.3	0.6	5.3	12.9	12.5	0.4	2.4	4.2	2.0	1.0	0.8	0.7	0.3	1.9	0.5	0.7	2.1	0.2	0.2	4.5061
		hepatocyte growth factor (HGF)	0.4	0.0	2.3	7.3	5.5	0.5	0.4	0.6	0.5	0.1	0.1	1.0	0.6	0.7	1.0	0.0	0.5	0.0	0.5	4.4335
		transcription factor BTEB2	0.1	0.2	7.5	14.3	22.1	23	2.0	4.9	3.7	1.2	1.3	1.5	2.5	1.4	0.5	0.2	1.1	0.9	0.8	4.363

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Fig. 6A-2

A. Basophil (Ba)-selective transcripts (2/2).

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Ba4 (small)	Ba5 (small)	Ba6 (small)	Ba7 (small)	Ba8 (small)
21451_S_at	U41813_1	class I homeoprotein (HOXA9)	0.6	1.7	6.3	8.3	0.3	0.8	0.5	1.0	0.7	0.7
32502_S_at	AL041124	DkrZp340316_S1 catenin (catenin-associated protein) alpha 2 FLJ22191	1.6	1.9	14.6	22.5	17.4	4.0	2.1	1.0	0.4	0.4
20337_S_at	NM_003891	AK026415_1	0.2	0.1	1.1	3.9	3.2	0.6	0.1	0.1	0.1	0.1
21967_S_at	NM_025231_1	beta2-chimera in ontostatin M	0.3	0.7	2.5	7.3	12.0	0.9	0.2	1.5	0.2	0.2
21338_S_at	AF1534192	keratin-associated protein	0.4	0.0	0.9	22.9	21.8	1.1	0.8	0.9	1.0	0.7
21463_S_at	NM_024837_1	FLJ1472 reino-like kinase	0.2	0.2	1.3	5.4	4.4	0.2	0.7	0.5	0.7	0.2
202490_S_at	NM_016231_1	FLJ1415 firs done MAAMA1002728	4.1	1.5	9.1	9.7	12.2	1.9	3.3	3.0	1.9	1.4
22941_S_at	NM_0162925	EL12 intronic transcript 1 mRNA	0.1	1.3	6.2	7.0	7.1	0.8	0.6	0.5	0.1	0.1
21200_S_at	AV708891	DkrZp340205	0.6	1.4	3.1	8.8	5.1	0.7	0.8	0.9	0.1	0.1
22230_S_at	AI138877_1	MAP kinase activating death domain in vets avian myeloblastosis virus E6	2.8	5.0	17.3	22.7	6.8	3.6	2.2	2.9	3.2	1.0
201664_S_at	AB0023561	MAP kinase activating death domain oncogene homolog 2	5.6	4.6	12.7	35.0	40.7	6.2	6.1	7.0	5.7	5.5
210252_S_at	AL575509	FLJ2876	1.7	0.1	18.4	34.7	50.7	2.8	1.6	1.7	0.9	0.5
201328_S_at	NM_022754	FLJ4110 firs clone MAAMA1003026	1.2	1.0	3.5	7.5	7.4	1.4	1.0	2.7	1.5	1.0
218392_X_at	NM_001813_1	GPR	0.0	0.3	15	8.1	13.1	1.7	0.5	1.9	1.2	0.9
205046_S_at	AF572230_1	histamine H1 receptor	0.6	0.8	3.9	3.4	3.2	7.8	11.9	8.7	9.3	10.0
221170_S_at	NM_0054961	chromosome-associated polypeptide C	2.2	4.3	17.6	15.1	18.1	3.4	6.6	4.9	4.2	4.0
208933_S_at	AI659005	lectin, galactoside-binding, soluble, 8 (galectin 8)	11.8	4.9	26.7	28.3	28.2	5.9	6.6	10.1	4.8	3.8
208710_S_at	AI563460	fatty-acid-binding protein 2 fatty-acid-Coenzyme A ligase very long-chain 1 (FACVL)	50.4	38.9	141.1	189.2	154.7	4.4	1.3	3.8	3.1	0.7
205760_S_at	NM_003645_1	KIAA0207	3.3	2.5	7.0	16.2	9.2	0.3	0.3	0.5	0.1	0.4
205249_S_at	D88962_1	KIAA0358	8.4	2.6	12.5	38.0	33.1	4.9	4.2	12.3	10.4	1.7
38398_S_at	AB02356	Ordin A1	5.5	4.1	13.8	24.6	29.8	6.1	6.4	5.6	7.0	3.0
208899_S_at	NM_003914_1	ADP-ribosylation factor-like 5	5.6	3.6	16.2	20.6	10.5	0.1	0.6	0.9	0.1	0.1
218150_S_at	NM_012097_1	zinc finger-related factor 1	8.2	5.3	31.6	56.6	54.6	9.1	8.6	14.0	12.1	3.9
213097_S_at	AI138837	oxysterol-binding protein-related protein	2.1	1.8	8.4	13.4	16.7	4.8	2.1	4.8	3.7	1.2
208150_S_at	NM_018630_1	nasopharyngeal carcinoma associated gene protein-8	1.2	2.3	8.8	18.0	15.3	0.6	0.8	1.5	2.3	2.7
210169_S_at	AF19492_1	FLJ20836	1.2	0.7	3.6	6.4	4.2	1.2	1.6	1.0	0.3	0.6
226918_S_at	NM_025143_1	am 1 (acetylmyeloid leukemia 1) oncogene	1.0	1.1	26.1	37.3	26.2	6.2	6.5	14.1	11.3	3.3
208359_X_at	I345981	exocyst complex NEF-sp	1.2	0.1	3.1	7.2	7.1	2.5	1.6	1.6	1.1	0.9
208107_S_at	NM_030941_1	DkrZp6401072	3.6	7.6	7.8	30.6	20.1	1.6	2.3	2.7	1.0	0.2
212412_S_at	AV775767	chromosome 16 BAC clone	18.2	16.2	41.3	72.5	67.3	7.7	16.3	11.6	6.4	9.1
215175_S_at	AC003481	CIT875K44H12	2.9	2.5	4.8	12.8	10.4	0.6	0.9	1.4	0.8	0.1
221505_S_at	AB014731_1	SMar-3	7.6	5.4	13.2	48.5	32.4	5.2	5.7	18.1	10.7	0.2
219837_S_at	NM_018439_1	hypothetical protein IMPACT	1.3	2.4	2.9	10.7	9.3	1.5	2.7	2.1	0.6	0.7
218352_S_at	NM_018191_1	KIAA0379	0.8	0.5	4.9	13.7	8.7	2.3	1.7	3.4	3.9	1.0
213035_S_at	AI081194	am 1 (acute myeloid leukemia 1) oncogene	2.1	3.8	11.1	26.7	22.4	2.5	1.5	1.9	1.1	0.3
211180_X_at	D89788_1	leth, galactoside-binding, soluble, 8 (galectin 8)	1.5	0.2	3.1	9.4	7.5	2.0	2.5	1.7	1.0	1.4
210731_S_at	AI136105	hypothetical Coenzyme A transporter	2.1	1.1	4.8	9.1	6.4	1.9	1.8	1.8	1.2	1.7
203164_S_at	BE64756	fatty-acid-Coenzyme A ligase very long-chain 1 (FACVL)	2.3	1.9	3.7	12.6	12.4	2.5	1.9	2.7	1.4	2.6
205768_S_at	NM_003645_1	Akt kinase (PKA) anchor protein (gravin) 12 Ca2+-independent phospholipase A2 short isozyme	3.0	1.7	3.9	10.7	7.7	0.4	0.1	0.6	0.7	0.1
210517_S_at	AB034761_1	25.1	4.9	44.0	69.5	59.6	15	0.4	0.6	0.8	0.5	0.1
210647_X_at	AF109881	23	1.1	18.7	13.2	9.1	3.4	3.3	4.0	45	33	5.0

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Fig. 6B

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Probe set	Accession #	Transcripts	NCI cord blood lung Ba1 (small)	NCI Ba2 (small)	NCI Ba3 (small)	NCI Eo (small)	NCI Eo (small)	Ne 1 (small)	Ne 2 (small)	Ne 3 (small)	Ne 4 (small)	CD4 CD8 CD14 CD19 Eb EsL							
207328_at	NM_0011401	15lipoxygenase	0.1 0.6	0.7	0.1	14.5	24.6	18.3	17.0	1.1	0.1	0.0 0.1 0.0 0.1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0							
219855_at	NM_04703.1	FJ22593	0.0 1.0	1.8	1.1	29.8	34.7	24.8	27.8	15	0.4	0.9 0.1 0.6 0.4 0.3 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1							
208353_at	NM_014421	R	1.3 2.4	0.4	0.2	17.1	23.1	17.6	11.8	0.4	0.1	0.8 0.3 0.2 0.1 0.2 0.5 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0							
211922_s_at	AY028632.1	soluble carrier family 29 catalase	3.7 2.2	62	68	22	78.2	134.5	119.7	88.8	162	13.0	8.8 0.7 2.2 2.9 11.1 7.5 4.6 9.125						
201802_at	NM_004955.1	CCAT enhancer binding protein (CEBP), epsilon	4.8 2.8	2.9	3.4	1.9	24.8	30.4	36.1	42.3	0.1	0.6	0.8 0.2 0.9 0.3 2.2 1.0 1.1 8.989						
214523_at	NM_001805.1	soluble carrier family 29 (nucleoside transporters)	0.1 0.1	0.7	1.2	1.2	7.9	11.4	23.4	17.3	1.8	1.5	1.9 1.1 1.4 0.5 0.4 1.0 0.1 0.1 0.1 8.9462						
210029_at	N34455.1	intereron-gamma-inducible indoleamine 23-dioxygenase	0.7 0.7	0.1	53	42	26	20.0	39.0	29.5	16	21	2.3 1.8 1.7 1.5 1.7 0.3 1.4 0.9 7.7078						
215573_at	AU147084	soluble carrier family 29 (fluoroacetate transporters)	0.1 0.1	0.7	0.3	1.1	9.8	8.4	16.9	7.2	0.4	1.9	1.8 0.7 2.0 0.1 0.1 0.4 0.0 0.0 7.5983						
201801_s_at	Af07117.1	oligodendrocyte lineage transcription factor 2	3.5 1.9	1.7	0.5	0.9	29.7	47.1	7.4	11.0	0.1	0.5	0.4 0.7 1.1 0.4 0.1 1.4 0.6 1.0 7.0314						
213825_at	AF221520.1	glucose-fructose oxidoreductase domain containing dachshund (Drosophila) homolog	0.4 0.6	0.2	0.4	0.6	60	10.9	18.7	12.5	0.8	0.9	1.5 1.0 0.6 1.7 0.3 0.4 0.3 0.3 6.5987						
219821_s_at	NM_018988.1	KIAA095	0.0 0.9	0.1	0.4	1.8	26	18.7	17.3	30.9	31.3	3.9	3.1 2.4 2.9 3.2 1.3 2.5 3.0 3.8 0.8 6.2284						
205472_s_at	NM_004929.1	chemokine CC23	0.6 0.6	1.8	0.4	1.1	0.5	55	62	12.6	85	13.5	10.6	0.2	0.1	0.1	0.1	0.1	0.0 6.0388
202188_at	NM_014659.1	lymphocyte membrane associated protein (LMP)	0.6 0.6	25	34	3.6	41.8	49.7	66.2	60.1	0.2	0.9	0.5 0.7 1.2 1.6 0.5 0.7 0.7 0.7 0.7 0.4 5.4499						
210548_at	U58913.1	ADORA3 adenosine A3 receptor	0.2 0.2	28	37	2.3	27	14	22	17.9	15	3.1	2.2 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1						
209447_at	AF43290.1	chemokine CC23	0.1 0.1	0.1	1.3	0.6	7.9	5.6	8.1	8.0	0.6	0.9	0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1						
206171_at	NM_0006772	transketolase-like protein	0.1 0.1	0.2	0.1	0.1	32	40	6.6	7.2	0.2	0.1	0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1						
210549_s_at	U58913.1	spectrin repeat containing, nuclear envelope 1	0.1 0.1	0.5	0.1	0.1	38	42	30	28	0.0	0.1	0.2 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1						
214183_s_at	X91817.1	PY22 purinergic receptor GPR	0.1 0.1	0.1	0.1	0.1	34	4.7	8.1	5.9	0.1	0.3	0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1						
215350_at	AB033088.1	thrombospondin 4 (THBS4)	0.1 0.1	0.1	0.1	0.8	32	5.9	10.0	6.4	1.8	1.4	0.6 0.9 0.3 0.2 0.3 1.4 1.1 1.2 1.1 1.1 1.1 1.1 1.1 1.1						
206377_at	NM_002564.1	L-iditol 2-dehydrogenase	0.1 0.1	0.1	0.1	12.8	22.5	29.9	49.0	37.0	13	3.0	4.4 2.2 21 1.6 1.2 2.7 2.5 1.8 4.1557						
204766_at	NM_003248.1	P2YX purinergic receptor GPR105 for UDP-glucose	0.8 0.8	0.1	15	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1						
201563_at	L29088.1	collagen, type X, alpha 2	4.1 2.6	35	11.4	12.8	22.5	29.9	49.0	37.0	13	3.0	4.4 2.2 21 1.6 1.2 2.7 2.5 1.8 4.1557						
206637_at	NM_0014879.1	PDZ domain protein	5.7 1.6	13.3	19.9	13.5	44.2	55.1	81.4	62.4	18	9.3	15.4 9.2 0.7 0.9 0.8 0.0 0.5 0.1 0.1 0.1 0.1 0.1 0.1 0.1						
213322_at	A173346.5	CD4 sigma transducer	0.1 0.1	1.9	1.9	1.3	10.3	9.5	6.6	8.8	2.7	2.1	2.1 2.2 0.7 1.2 1.2 1.2 1.2 0.9 3.8576						
214705_at	A001306.1	catalogue of life	0.1 0.1	0.4	0.3	0.1	2.1	15	21	22	0.3	0.0	0.0 0.0 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3						
266_s_at	L33930	CD4 sigma transducer	0.2 0.2	3.0	0.3	0.8	11.9	14.0	18.8	13.9	0.1	0.3	0.8 0.9 0.0 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1						
204322_at	NM_001752.1	cathepsin D	23.0 14.3	35.7	49.4	19.9	20.3	20.7	22.1	6.0	5.0	5.3	71.3 60.9 92 11.2 15.1 53.6 299 24.4 33.325 3.3203						
205696_at	D26054.1	fuctose-1,6-disphosphatase	0.9 3.4	43	11.1	64	20.2	27.7	28.8	32.5	30	2.5	24 15 19 20 1.6 8.1 1.1 0.6 3.3089						
216379_x_at	AK000168.1	CD4 sigma transducer	1.3 1.4	16.2	0.9	15	66.1	70.1	81.9	77.9	1.7	2.8	2.6 4.1 4.8 0.5 0.6 0.9 2.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5						
205569_at	NM_014398.1	lysosome-associated membrane glycoprotein (LAMP4)	0.4 0.2	0.7	0.1	0.4	24	31	6.8	3.0	0.6	0.1	1.4 0.8 0.4 1.1 0.7 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1						
219333_s_at	NM_018530.1	hypothetical protein PHO221	0.1 0.1	2.1	4.6	5.4	75	85	21.8	21.2	0.3	0.1	1.7 2.1 0.1 1.7 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1						
202286_s_at	J04152	gastrointestinal tumor-associated antigen (GATA3)	0.9 0.9	0.7	1.3	0.3	0.1	1.1	2.5	8.7	1.8	0.4	0.8 0.6 0.2 0.2 0.2 0.2 0.2 0.2 0.2 0.2 0.2 0.2 0.2						
205442_at	NM_003107.1	semenogelin I (SEMG1)	0.6 0.6	0.1	0.4	0.0	0.1	1.2	3.2	4.9	3.4	0.3	0.1 1.9 0.1 0.2 0.2 0.9 0.4 0.4 0.4 0.4 0.4 0.4 0.4						
205733_at	NM_0008557.1	Bloom syndrome	1.9 1.1	2.0	2.4	2.2	8.5	6.0	7.5	11.2	2.1	2.0	1.0 1.2 1.2 2.4 1.8 1.1 2.6 1.2 3.1427						
204392_at	NM_0036562	calcium/calmodulin-dependent kinase (CAMK1)	4.0 1.1	63	89	64	17.8	19.3	24.9	26.5	0.6	0.2	1.8 1.5 0.1 1.4 1.0 3.0 0.6 0.6 0.6 0.6 0.6 0.6 0.6						
213497_at	AL053374.1	DKEZ2	1.0 0.7	1.0	1.3	1.6	63	68	60	23	3.0	1.4	2.3 2.0 0.4 0.5 1.6 1.7 1.1 1.1 1.1 1.1 1.1 1.1 1.1						
219296_at	NM_019028.1	similar to argyrophilic repeat-containing protein ARRI	2.2 1.7	0.2	3.5	1.6	7.3	4.4	8.4	7.4	1.8	2.4	2.3 0.1 1.4 1.6 1.3 1.9 0.8 0.8 0.8 0.8 0.8 0.8 0.8						

Fig. 6C

B. Eosinophil (Eo)-selective transcripts (1/1).

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C. Neutrophil (Ne) selective transcripts (1/7).

Probe set	Accession #	Transcripts	MC	cord	MC	blood	lung	Ba 1	Ba 2	Ba 3	Eo	Eo	Eo 3	Eo 4	Ne	Ne	Ne 3	Ne 4	CD4	CD8	CD14	CD19	Fb	Ne S1			
				(small)	(small)			1	2	(small)	1	2	(small)	1	2	(small)	1	2	(small)	1	2	1	2				
205403_at	NM_004633.1	R	IL12B	Interleukin 1R type II	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	12.786			
216732_at	AK026679.1		KCNJ15	inward rectifier potassium channel K _{ir} 1.13	0.7	1.1	0.1	0.1	0.0	0.0	0.6	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	11.228		
210119_at	U73191.1	ICN	chitinase-like 1 (cartilage chitinase-like 39)	1.5	0.2	0.9	0.1	0.4	0.3	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.0	10.747	
209395_at	M80927.1		glucoprotein inhibitor 3, skin-derived (SKALP)	0.2	0.1	0.1	0.1	0.8	0.5	0.2	0.4	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	51.901	
203691_at	NM_002638.1																										
211372_s_at	U64094.1	R	Inhibitor 1R type II	0.1	0.2	0.1	0.1	0.0	0.0	0.1	0.0	0.1	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	50.606	
207098_at	NM_001557.1	GPR	OCR2	Interleukin B receptor, beta	0.0	0.4	1.1	1.2	1.0	1.3	1.3	2.1	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	39.316
206515_at	NM_000896.1	R	leukokinase B4 omega hydroxylase (CP4E3)	0.3	0.1	1.1	0.7	1.2	0.5	0.8	0.5	0.9	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	34.919	
204007_at	J04621.1		FC gamma RIIb (CD16)	0.8	0.7	1.4	1.6	1.8	1.7	1.8	2.8	1.9	2045	2265	1940	1733	166	13	22	26	26	26	26	26	26	26	28.895
204470_at	NM_001511.1		melanoma growth stimulating activity, alpha	1.2	0.0	0.7	0.9	0.1	0.6	0.5	1.2	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	28.189	
206025_s_at	AW188198		tumor necrosis factor,	0.1	0.3	0.1	0.6	0.4	0.6	0.1	0.2	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	26.336	
209396_s_at	M80927.1		alpha-induced protein 6, chitinase 3-like 1 (cartilage chitinase-like 39)	1.8	0.2	1.6	0.4	0.5	0.8	0.5	0.6	0.9	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	22.254	
211865_s_at	D87291.1		mitochondrial split pore potassium channel K _m 3	0.9	1.7	2.0	1.4	1.4	2.1	1.3	1.8	1.7	6.2	7.72	7.75	56.8	3.0	1.0	1.1	1.7	0.9	0.9	0.9	0.9	0.9	20.163	
221920_s_at	BE57761		mitochondrial split pore carrier	0.4	0.8	0.9	0.0	0.2	2.4	1.5	2.2	1.5	59.0	43.2	57.4	46.8	25	0.7	0.3	1.8	1.1	1.0	1.0	1.0	1.0	18.973	
207094_at	NM_000624.1	GPR	CYCRA1	Interleukin B receptor, alpha	0.3	0.1	42	43	44	0.3	0.3	0.2	0.3	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	19.325
213559_s_at	AW468201		23614 mRNA sequence	0.0	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	18.973
218982_s_at	NM_0015515.1		DKFZP434G052	0.0	0.1	0.5	0.3	0.1	1.1	2.8	2.8	2.0	46.3	32.5	40.3	31.3	3	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	18.3	
213506_at	BE955369	GPR	PAR2	PAR2 proteinase activated receptor-2	0.1	0.0	0.0	0.4	0.3	1.2	1.3	4.1	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	15.913
220187_at	NM_024636.1		FEZ1	alpha-induced protein 6, tumor necrosis factor	0.3	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	18.208
206026_s_at	NM_007115.1		alpha-induced protein 6, elafin	0.1	0.8	0.4	0.8	0.6	1.1	0.5	0.9	0.7	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	17.051	
414658_at	L10343		equipotin 9	0.12	0.7	1.2	0.8	0.8	0.9	1.0	0.7	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	13.337	
210482_s_at	BC056943.1	R	decay receptor 1, TNFRSF1B	0.7	0.7	0.4	0.4	0.7	1.7	4.9	0.9	0.9	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	12.744	
215223_s_at	W26388		superoxide dismutase 2	0.4	1.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	12.024	
210484_s_at	BC056943.1	R	decay receptor 1, TNFRSF1B	0.9	0.9	0.9	0.9	0.2	2.2	4.8	0.8	0.8	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	11.779	
205654_at	NM_000715.4	GPR	complement component 4-binding protein, alpha	0.5	1.1	1.3	0.7	0.7	1.5	1.0	1.3	1.4	2.1	2.07	43.6	33.7	12	0.3	1.3	1.2	1.2	1.2	1.2	1.2	1.2	12.161	
210773_s_at	U81501.1		formyl peptide receptor 2	0.8	0.1	0.6	0.6	0.3	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	12.14	
206222_at	NM_004684.1	R	decay receptor 1, TNFRSF1B	1.5	0.8	1.9	0.7	0.7	3.6	13.7	3.4	3.4	3.9	1210	1371	375	59.9	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	10.618	
202088_s_at	NM_003003.1		SEC45 (ceramide-like 1)	0.8	0.2	0.9	1.8	3.0	22	26	38	26	36	25.9	33.9	326	1.3	0.1	0.1	0.1	0.1	0.1	0.1	0.1	10.418		
211163_s_at	AF012536.1	R	decoy receptor 1, TNFRSF1B	0.2	0.1	2.2	15	0.6	2.6	12.3	9.4	6.4	8.79	10.9	60.4	55.8	0.5	0.2	0.1	0.7	0.1	0.6	0.1	0.6	10.404		
205931_s_at	NM_004904.1		cAMP response element-binding protein CREBPa	0.0	0.1	0.3	0.1	0.6	0.6	0.6	0.6	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	10.451	
205922_at	NM_004665.1		vanin 2	0.1	0.0	1.2	2.6	3.9	1.0	0.2	1.9	0.3	1.45	114.6	174.1	189.2	0.1	1.4	4.0	13.8	1.7	0.0	0.0	0.0	10.451		
210176_at	AL050621	R	Toll-like receptor 1	0.7	0.6	0.2	0.3	0.3	0.5	1.1	1.9	0.9	1.2	295	386	251	326	1.6	0.8	0.7	3.0	1.5	0.3	0.3	0.3	10.203	
215977_X_at	X68185.1		glyceraldehyde-3-phosphate dehydrogenase	1.9	0.9	0.8	0.7	0.9	0.7	0.9	0.9	0.9	1.0	158	198	97	109	0.1	0.1	0.2	0.2	0.2	0.2	0.2	0.2	10.167	
215783_s_at	X14741		GK gene for glycerol kinase, exon 1	0.5	1.2	0.7	0.7	0.9	0.4	0.5	0.5	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	10.067	
217677_X_at	AJ25250		KIAA0779	1.2	0.1	0.2	0.3	1.0	0.2	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	12.9774	
213349_at	A1934439			0.9	0.7	1.4	1.4	1.0	1.9	0.9	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	12.9774	

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Fig. 6D

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C. Neutrophil (Ne)-selective transcripts (2/7).

Probe set	Accession #	MC	MC cord blood	MC lung	Ba1 (small)	Ba2 (small)	Eo (small)	Ne (small)	Ne4 (small)	Ne (small)	Ne3 (small)	Ne2 (small)	Ne1 (small)	p1	CD4	CD8	CD14	CD19	Fb	Ne51			
210789_X_at	U005621	GPR	Transcripts	1.1	0.4	1.9	1.5	2.0	1.5	2.5	0.4	1.94	18.6	22.6	155	0.7	1.6	0.9	2.0	0.3	1.1	92749	
210792_at	M881071		carinoembryonic antigen (CEA)	0.1	0.2	0.4	0.7	0.7	0.3	0.8	0.7	51.4	67.7	44.8	46.4	0.5	0.5	0.5	0.5	0.1	0.1	92661	
218972_S_at	NM_016586.1	R	formyl peptide receptor 2	0.7	0.5	1.6	0.2	0.5	1.1	0.9	0.7	0.5	26.3	20.5	6.6	28.0	0.7	0.4	1.1	0.2	0.4	0.4	91536
204006_S_at	NM_009570.1	R	F-gamma R IIIb (CD16)	0.7	0.2	1.2	0.7	0.6	0.7	0.8	0.7	0.7	230.7	278.8	47.6	45.9	42	1.9	6.9	12.0	3.9	0.1	90769
202725_S_at	NM_001995.1		fatty-acid-Coenzyme A ligase, long-chain 1 (FACL1)	4.3	2.6	5.1	11.5	19.4	5.3	5.1	3.7	93.8	127.8	92.8	69.1	0.7	1.0	1.1	83	0.9	1.7	89855	
220302_at	NM_0055962		male germ cell-associated kinase	0.1	0.0	1.3	0.7	0.8	0.7	0.2	2.0	14.7	84	7.9	8.9	0.3	0.1	0.1	0.0	0.1	0.0	88366	
221803_S_at	AA0883074		nuclear receptor binding factor-2	1.1	0.8	3.2	4.0	2.9	2.8	2.8	4.7	3.2	24.7	25.2	33.2	29.3	0.1	1.2	1.7	2.0	2.6	8.3788	
206765_at	AF153820.1	IgN	KCNQ inwardly-rectifying potassium channel Kir2.1	1.0	0.4	2.5	4.4	2.4	4.7	6.1	8.0	25.8	36.2	52.4	48.3	0.4	0.2	0.5	1.5	0.7	1.1	8108	
213357_S_at	AI934469		ubiquitin-conjugating enzyme E2D1	0.0	0.1	0.9	2.0	1.6	0.8	0.6	2.3	2.7	7.9	5.9	20.1	18.0	0.2	0.5	0.2	1.2	0.2	7.9705	
214590_S_at	AI545760		leukotriene B4 omega hydroxylase (CYP4F3)	0.1	1.5	0.3	0.4	0.5	1.1	1.0	0.5	0.4	7.9	10.7	10.1	4.4	0.1	0.4	0.3	1.0	0.4	0.9	7.8712
206522_at	NM_004668.1	R	leukotriene B4 omega hydroxylase (CYP4F3)	0.0	0.0	0.8	1.8	1.0	3.0	5.4	11.7	9.4	46.0	51.5	56.9	43.0	0.1	0.0	0.0	0.6	0.6	0.1	75773
210992_X_at	U90939.1		Fc gamma receptor IIc2	1.9	1.0	1.7	2.1	3.3	8.1	16.1	2.8	42	70.9	95.6	42.8	30.5	0.3	0.2	0.1	7.2	2.3	0.2	75239
220528_at	NM_018399.1		VNTR protein	0.1	0.2	1.3	6.1	5.0	0.2	0.1	0.5	0.4	26.8	22.1	20.0	36.8	0.8	0.2	0.1	3.0	0.1	0.1	75216
200919_at	NM_004227.1		early development regulator 2	5.6	4.4	4.8	6.5	9.6	7.6	6.8	5.3	7.3	109.5	89.0	52.9	61.4	2.5	4.9	7.0	10.0	3.9	6.5	75056
203781_S_at	NM_000167.1		glucokinase	2.1	1.5	1.0	1.5	1.6	1.1	1.4	1.6	1.4	14.3	20.3	10.7	10.3	0.9	0.6	0.3	1.7	0.6	0.6	74603
117_at	X51757		heat-shock protein HSP70B	1.1	0.2	0.8	0.6	0.9	0.5	0.8	2.1	4.1	46.3	41.2	25.1	25.8	0.4	0.9	0.6	3.7	1.6	0.5	74139
205774_S_at	NM_012413.2		glutaminyl-peptide cyclotransferases triggering receptor expressed on myeloid cells 1	0.4	0.0	0.4	0.7	0.9	0.7	0.0	0.4	0.3	30.1	47.7	36.4	24.7	0.7	0.6	0.6	4.6	0.1	1.5	73246
219434_at	NM_018643.1		thrombomodulin	1.3	0.3	0.4	0.2	0.5	2.9	0.7	1.4	1.5	92.8	84.0	81.2	98.6	3.4	0.6	0.1	12.3	0.9	0.3	72368
203881_S_at	NM_000361.1		transmembrane domain 1 (ORM1)	1.7	0.1	0.4	0.4	0.4	0.2	1.0	1.4	1.1	16.8	13.0	13.4	13.3	0.7	0.6	0.4	1.1	0.4	0.2	71328
203040_at	NM_000607.1		transmembrane domain 1 (ORM1)	0.5	0.1	0.1	0.4	0.1	0.1	0.0	1.1	0.0	3.4	4.1	4.3	0.7	0.1	0.3	0.1	0.4	0.0	0.2	70823
214681_at	A1830490		glucokinase	0.2	0.4	0.1	1.2	1.7	0.8	1.1	0.6	1.2	7.8	14.2	24.0	12.1	0.9	0.0	0.1	1.9	1.0	0.3	6986
218033_S_at	NM_019027.1		FLJ20273	2.9	1.0	0.9	1.5	0.8	0.9	0.4	1.3	1.1	47.2	54.4	91.9	94.0	1.7	0.7	0.4	9.9	1.5	0.3	69074
203068_S_at	BE571084		GTPase regulator associated with the focal adhesion kinase ppi25(FAK) secretory leukocyte protease inhibitor (antileukoproteinase) (SLPI)	1.2	1.4	3.5	5.1	5.1	5.1	8.5	7.1	43.7	40.6	45.2	56.0	0.7	1.3	2.9	5.1	0.8	1.2	68934	
203021_at	NM_003064.1		diacylglycerol acyl transferase	1.7	0.8	4.6	1.5	1.1	1.2	2.2	8.5	0.8	162	19.8	13.9	8.7	1.8	0.6	1.2	1.7	1.1	2.1	67497
216316_X_at	X787713		diacylglycerol acyl transferase 1	2.0	0.9	0.4	0.6	1.0	0.7	0.6	0.5	1.0	10.3	18.6	5.8	5.8	0.5	0.2	0.2	0.8	0.3	0.1	66675
217209_at	X16454		carinoembryonic antigen subdomains A and B	0.6	0.4	0.2	0.2	0.4	0.1	0.3	0.7	0.5	28	38	33	2.7	0.3	0.4	0.0	0.1	0.1	0.2	65382
220421_at	NM_024850.1		FLJ21458	0.3	0.6	0.1	0.1	0.1	0.1	0.3	0.8	0.4	0.3	89	72	9.1	7.0	12	0.6	0.0	0.1	0.2	64837
213524_S_at	NM_015714.1		putative lymphocyte G0/G1 switch gene (G022)	0.8	0.8	1.3	0.9	0.5	0.8	0.5	18.7	10.1	118.0	52.0	39.6	92.5	1.7	0.8	0.1	6.0	0.2	3.4	64779
208472_S_at	NM_005078.1		transducin-like enhancer of split 3	2.2	2.6	1.3	0.7	0.5	1.6	0.6	0.5	1.0	22.6	25.0	11.3	83	13	12	1.5	18	15	0.9	64334
212765_at	AI567426		KIAA01547	1.4	1.5	0.5	1.3	2.3	1.1	1.0	2.2	1.9	17.9	15.9	15.1	128	24	0.8	1.1	1.3	1.2	0.5	64271
204307_at	AB002295.1		KIAA0339	0.7	0.0	0.1	2.6	2.1	1.8	1.5	2.4	20	10.3	11.2	154	128	19	0.1	0.5	0.2	0.1	0.5	63478
203591_S_at	NM_000760.1	R	granulocyte colony-stimulating factor receptor	0.1	0.0	1.0	0.1	0.2	2.3	0.6	2.4	1.0	220.3	187.2	134.9	112.1	0.2	0.8	0.2	25.5	0.1	0.2	62051
210210_at	AF181660.1		immunoglobulin superfamily member WM78	0.9	1.1	1.6	1.8	1.9	1.1	1.9	1.7	20	11.1	7.0	13.7	14.1	1.4	1.3	0.9	1.6	1.1	0.6	6172
218610_S_at	NM_018340.1		FLJ1151	1.5	1.2	1.2	1.2	1.8	3.3	3.2	2.6	18	252	23.3	17.9	21.8	0.5	0.6	0.4	3.6	0.4	0.6	6112
203561_at	NM_021642.1	R	Fc gamma receptor IIa (CD32)	4.7	1.2	0.9	1.2	2.4	1.95	22.8	19.4	21.4	104.3	129.0	153.0	123.9	40	0.7	1.63	22	0.2	61015	
216841_S_at	X15132.1		superoxide dismutase 2	1.3	1.1	1.2	1.8	2.2	1.4	1.3	32	24	20.5	44.6	35.8	42.2	56	0.8	0.7	20	0.7	1.1	6024

Fig. 6E

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C. Neutrophil (Ne)-selective transcripts (3/7).

ProbeSet	Accession #	Transcripts	NC cond	MC	Ba1	Ba2	Ba3	Eo	Eo	Eo	Eo	Ne	Ne	Ne	Ne	pl	CD4	CD8	CD14	CD19	Fb	NeS.I.		
			blood	lung	Ba1 (small)	Ba1 (small)	Ba1 (small)	1	2	(small)	1	2	(small)	1	2	(small)	1	2	(small)	1	2	(small)		
207624_S_at	NM_0013281	retinitis pigmentosa GTPase regulator RPE65	0.0	0.6	1.1	2.0	1.2	1.1	1.2	2.1	2.8	7.1	7.0	13.6	15.1	0.2	12	0.4	0.9	0.7	0.3	6.0348		
209850_S_at	BC005406.1	Cdc22 effector protein 2	0.2	0.2	1.3	0.2	1.0	0.2	0.4	0.5	0.4	132	96	67	87	0.2	0.2	0.2	0.2	0.6	0.4	0.4	5.9313	
209365_S_at	NM_004994.1	matrix metalloproteinase 9	47.7	0.6	1.6	1.9	1.4	1.2	2.4	15.5	15	365	351	368	219	17	20	1.4	1.9	1.3	1.4	1.4	5.9311	
215962_X_at	AA292874	glycerofatty acid ester hydrolase	12	0.2	0.6	0.1	1.2	0.2	1.0	1.2	6.6	102	73	74	0.2	0.1	0.1	0.2	1.3	0.5	0.5	0.0	5.9077	
206925_at	NM_005668.1	sialyltransferase 8	3.1	1.2	2.1	2.5	2.0	1.4	3.1	1.6	21.7	333	68	114	0.4	0.9	1.6	2.6	12	0.2	12	0.2	5.8688	
211762_S_at	BC009980.1	ubiquitin-conjugating enzyme EDD1	1.8	1.4	1.1	2.9	2.4	2.5	5.7	3.9	22	293	312	526	254	0.2	2.0	1.4	5.7	13	2.3	13	2.3	5.8143
201192_S_at	NM_006224.1	phosphotyrosyl-phosphotyrosine transfer protein (PTTP1)	30	3.1	1.9	5.0	4.6	3.9	5.4	6.6	54	27.9	26.9	329	352	2.0	3.5	3.7	5.0	3.2	2.8	3.2	2.8	5.811
205921_S_at	U16120.1	placental lactate transporter	1.2	0.7	0.5	0.2	0.4	0.3	1.6	0.5	0.9	148	172	28	256	0.0	0.1	0.3	1.1	0.3	0.4	0.3	0.4	5.7909
209137_S_at	BC00263.1	ubiquitin C-terminal hydrolase related polypeptide	3.6	4.1	2.0	2.6	1.9	1.5	0.9	2.7	0.9	25.0	24.5	37.6	287	3.5	5.0	2.5	3.5	2.7	3.0	2.7	3.0	5.7864
208052_X_at	NM_001815.1	cathepsin B-like antigen-related cell adhesion molecule 3 (CEACAM3)	1.7	1.4	2.9	2.7	1.9	3.0	2.6	2.8	2.1	14.3	16.5	200	137	2.5	1.3	2.3	2.8	2.5	1.6	2.5	1.6	5.7572
203395_S_at	NM_00876.1	R	6.4	2.8	0.2	0.8	1.8	4.1	5.4	6.8	54	874	1069	801	717	1.7	2.9	8.7	8.4	4.8	4.8	1.3	1.3	5.6442
218614_at	NM_018169.1	insulin-like growth factor 2 receptor FJU1062	1.2	1.0	6.9	13.7	12.5	32	7.7	5.8	52.7	54.4	82.8	83.9	29	87	11.8	32	10.8	13	1.3	1.3	5.6443	
200842_S_at	NM_00303.1	SEC14 (S. cerevisiae) like 1	5.7	2.5	12.8	28.8	22.6	20.6	18.7	35.5	295	1307	1297	1356	1779	192	47	3.5	11.5	7.7	11.8	11.8	5.6348	
320659_at	AB014515	KIAA0615	2.8	1.5	2.1	5.6	5.5	4.6	3.7	5.9	69	23.9	20.9	35.1	40.5	1.0	3.4	3.3	2.6	2.1	2.1	1.5	1.5	5.6348
205896_at	NM_003059.1	solute carrier family 22 member 4 (SLC22A4)	0.8	1.2	1.0	0.1	1.1	1.9	2.4	3.5	2.7	85	13.3	30.0	126	0.5	0.7	0.8	2.6	0.5	1.4	1.4	1.4	5.4612
205894_at	NM_015364.1	MD-2 protein	7.4	1.1	2.0	3.9	2.2	1.5	5.4	12.3	84	40.2	57.3	54.9	60.9	3.8	0.8	1.3	2.7	1.1	3.5	9.4	9.4	5.4449
202082_S_at	NM_003093.1	SEC14 (S. cerevisiae) like 1	1.9	0.3	3.6	2.5	2.2	1.5	5.4	12.3	84	40.2	57.3	54.9	60.9	3.8	0.8	1.3	2.7	1.1	3.5	2.4	2.4	5.4422
203438_S_at	NM_014844.1	KIAA0329	2.9	1.1	2.2	2.8	2.1	3.1	3.1	3.1	43	165	187	199	190	34	1.3	1.7	1.8	1.3	2.5	5.4369		
205700_at	NM_004347.1	caspase 5	0.3	1.1	0.1	0.0	0.1	0.1	0.3	0.2	0.5	42	62	4.6	2.9	0.3	0.4	0.8	0.1	0.3	0.3	0.3	5.3179	
203435_S_at	NM_007287.7	CD10 membrane metallo-endopeptidase	0.3	0.5	0.4	0.3	0.2	0.1	0.3	0.3	0.2	164	44.2	54.6	42.8	0.2	0.2	0.2	0.2	0.2	0.2	0.9	0.9	5.2591
205539_at	NM_006276.1	ashillin	0.4	0.5	2.0	1.4	0.8	1.0	1.1	1.1	84	69	60	101	1.0	1.3	0.4	1.5	0.7	1.1	1.1	1.1	5.2541	
204601_at	NM_014664.1	KIAA0615	1.9	1.2	1.3	3.2	2.3	3.0	2.7	3.7	30	129	128	202	200	0.7	2.2	2.6	1.3	1.9	1.0	1.0	1.0	5.2381
201963_S_at	NM_0211222	long-chain 1 (FAT1)	29	2.1	5.0	19.9	33.4	6.6	3.8	10.3	61	58.8	86.6	922	802	0.1	1.1	1.1	10.8	1.5	2.4	1.5	2.4	5.2374
207064_S_at	NM_009590.1	GPR	0.7	0.1	0.9	0.9	0.8	0.8	0.8	0.9	12	4.3	4.7	4.0	6.6	0.8	0.5	0.8	0.5	0.8	0.3	0.3	0.3	5.1905
220005_at	NM_023914.1	GPR	0.6	0.0	0.1	0.5	0.1	1.97	96	25.1	173	765	77.1	1007	98.6	19	0.1	0.2	123	0.6	0.6	0.6	0.6	5.1686
211395_X_at	U93940.1	R	4.6	0.3	7.3	9.7	15.1	9.7	19.5	44	66	1150	1403	42.9	38.9	30	1.4	0.6	14.0	7.2	7.2	7.2	7.2	5.1401
201780_S_at	NM_007782.1	ring finger protein 13 (RNF13)	4.4	2.8	3.5	9.2	6.6	6.8	6.2	8.9	7.1	27.1	36.6	52.5	35.7	0.8	4.1	3.7	1.9	2.9	2.5	2.5	2.5	5.1047
209844_at	AB04511&1	GSK-3 binding protein FRAT2	2.8	1.3	4.4	9.2	8.0	13.4	16.9	27.3	22.6	93.2	97.2	100.6	104.2	1.3	1.9	1.9	1.9	1.9	1.9	1.9	1.9	5.1043
218199_at	NM_020651.2	pellino (Drosophila) homolog 1 (PELL1)	3.4	2.9	5.9	17.5	33.5	17.7	11.7	12.6	15.1	64.9	88.3	73.0	80.2	24	6.3	2.9	13.8	12.6	1.1	1.1	1.1	5.0277
206632_S_at	NM_004960.1	phorbolin	0.6	1.1	1.0	1.2	2.6	1.3	0.8	3.9	0.5	19.6	11.1	30.8	0.5	15	0.2	0.4	0.4	1.0	1.2	1.2	1.2	4.9858
220590_S_at	NM_038938.1	DKEZ3p566133	11.7	6.2	4.6	18.5	12.5	5.0	3.3	8.2	49	1155	1172	125.3	122.5	26	53	42	24.1	4.4	8.3	4.4	8.3	4.9332
204748_at	NM_00963.1	COX2 prostaglandin-endoperoxide synthase 2	6.5	16.2	6.6	24	20	45	23	34	35.8	44.1	44.6	91.8	0.4	0.6	0.2	4.3	0.3	0.5	4.9206			
210423_S_at	L32788.1	integral membrane protein	2.0	0.2	1.4	1.6	1.3	1.3	1.2	1.2	1.2	1.2	1.2	1.2	1.2	0.2	0.2	0.2	1.5	1.0	1.0	1.0	1.0	4.9845
206429_at	NM_0052422	PAR2 protease activated receptor-2	0.8	0.8	0.9	0.2	0.9	0.2	0.2	0.2	0.8	0.8	0.8	0.8	0.8	0.2	0.2	0.2	0.2	0.3	0.7	0.3	0.7	4.8608
213352_at	AJ54469	KIAA0779	0.6	0.9	1.2	1.5	1.2	1.2	1.5	1.5	22	84	60	87	77	1.6	0.9	1.5	1.5	1.0	1.3	1.3	1.3	4.8373
201888_S_at	U813793	R	0.1	0.3	0.2	0.0	1.7	1.7	1.7	1.7	20	86	19.0	15.0	13.9	0.4	0.3	0.3	0.3	2.9	1.3	1.3	1.3	4.746

Fig. 6F

C. Neutrophil (Ne)-selective transcripts (4/7).

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo	Eo3 (small)	Eo4 (small)	Ne	Ne3 (small)	Ne4 (small)	CD4	CD8	CD14	CD19	Fb	BaSL
20780_s_at	AA16751	R	CD95/Fas/APO-1	1.4	7.2	1.0	1.5	6.6	6.7	9.3	6.6	453	303	1.3	5.6	4.8	3.6	9.7	47254
209310_s_at	U25804.1	Irr-2 cysteine protease phosphatidylinositol glycan class B (PIGB)	2.5	1.9	2.1	7.7	7.0	1.4	1.3	1.3	1.4	19.1	17.5	2.3	2.9	4.1	4.5	3.9	22
205452_at	NM_004855.1	FLJ28950	2.3	2.7	2.3	6.4	7.7	2.3	1.4	3.0	3.0	16.3	17.6	2.2	3.93	1.7	2.9	3.5	22
218298_s_at	NM_024952.1	swinealpha/neuraminidase	3.1	3.3	5.4	8.1	7.2	5.7	5.7	8.8	9.4	37.2	23.4	3.73	39.1	0.6	1.7	3.1	27
221205_s_at	NM_030769.1	chromosome 1 open reading frame 12 clone MGC12484	3.8	12	0.8	1.2	1.4	3.0	4.7	3.2	4.6	20.4	23.6	2.35	18.3	0.6	0.7	0.3	0.5
221497_x_at	BC005369.1	fermin/light peptide-like 1	3.0	24	4.3	5.7	5.9	3.3	7.6	7.9	5.4	29.3	32.4	24.3	21.5	1.8	3.1	2.9	1.9
204668_at	AL031670	quanine nucleotide binding protein 10 (GNAT10)	0.8	0.5	1.8	1.0	1.2	0.3	1.5	1.7	0.9	8.4	8.1	7.0	6.5	1.4	1.3	1.0	1.6
201921_at	NM_004125.1	peroxisomal acyl-coenzyme A oxidase	7.1	5.4	2.6	6.7	6.5	11.7	11.4	20.8	15.3	45.5	87.5	81.3	57.1	0.8	2.7	3.0	8.4
209600_s_at	S69189.1	GPR	2.9	1.7	2.8	5.3	4.7	1.4	1.0	1.2	1.3	15.0	17.7	21.4	21.2	0.4	1.0	0.8	2.1
205119_s_at	NM_002029.1	formyl peptide receptor 1	4.1	1.4	11.2	26.6	32.7	14.0	11.1	4.2	6.0	288.2	315.8	274.7	25.9	3.6	1.3	0.7	1.7
217738_at	BF575514	pre-B-cell colony enhancing factor	5.7	0.9	7.4	24.1	34.9	7.5	4.6	5.1	3.9	73.4	87.0	89.9	79.9	2.2	1.7	1.6	1.7
215058_at	AL020388.1	DKEF2564AM2422	0.0	0.1	0.0	0.1	0.4	0.9	0.5	0.8	0.3	7.1	12.9	4.5	7.9	0.1	0.5	0.5	0.1
207555_s_at	NM_003744.1	numb	0.7	1.1	1.1	2.5	2.4	1.7	1.8	2.9	1.2	11.2	10.5	7.4	0.8	0.5	0.5	1.6	
213418_at	NM_002155.1	heat shock 70D protein 6 (HSP70B)	1.1	0.4	0.7	1.5	1.6	25.3	28.8	10.5	17.0	104.0	91.6	70.8	70.5	1.1	1.1	1.2	
218233_s_at	NM_016605.1	putative nuclear protein (LOC13077)	5.7	3.8	6.6	13.0	12.6	8.5	10.3	13.0	10.9	40.1	39.7	47.0	59.7	3.0	4.4	5.9	4.7
210356_s_at	BC001906.1	Similar to mitoch 1	6.2	1.9	2.7	5.4	4.0	1.4	2.2	1.8	3.6	19.5	15.8	23.4	23.8	2.6	4.1	5.0	6.0
207643_s_at	NM_001005.1	CD120a, TNFRSF55	1.8	1.6	0.9	1.3	1.4	0.9	1.4	0.9	1.0	81.1	83.6	68.6	65.6	1.3	2.2	5.9	17.4
203140_at	NM_001706.1	B-cell lymphoma 6 (BCL6)	6.2	2.9	9.1	13.5	19.8	23.5	16.7	28.7	33.1	99.1	107.8	115.8	101.1	2.2	3.4	3.4	6.7
207233_s_at	NM_016936.1	ubiquitin C	3.2	2.8	2.9	4.4	5.0	3.8	2.6	3.8	3.6	16.7	20.0	14.2	17.8	2.3	2.5	2.5	2.4
202875_s_at	BE97715	pre- β -cellular keratin transcription factor 2	2.0	1.4	0.1	0.1	0.2	2.5	3.6	2.1	1.5	11.6	15.4	6.8	7.5	0.8	1.7	1.9	1.3
218791_s_at	NM_024713.1	FLJ22557	1.2	0.7	2.5	2.7	1.8	0.9	1.5	1.6	1.0	6.9	8.7	36.1	37.9	3.1	6.8	8.7	10.1
211822_X_at	AF05451.1	Usuin-beta bromodomain adjacent to zinc finger domain, 1A	3.5	2.6	16.8	9.7	10.1	5.6	10.2	7.7	7.1	65.7	67.7	36.1	37.9	3.1	6.8	8.7	20
217986_s_at	NM_013448.1	KIAA0933	3.5	3.0	3.5	9.2	8.4	6.1	8.5	14.5	13.1	39.0	35.1	43.5	51.6	2.5	5.9	6.5	5.0
217965_s_at	NM_022083.1	CASP8 and FADD-like apoptosis regulator (CFAR)	2.3	3.5	0.4	0.9	1.1	0.8	0.6	0.4	0.8	17.1	18.1	12.9	13.4	1.5	0.5	0.3	0.8
208485_X_at	NM_003879.1	gp 180-carboxy peptidase D-like enzyme	3.2	2.5	19.2	9.8	9.9	6.2	13.0	8.1	8.3	70.8	69.7	33.8	41.4	3.5	6.4	8.4	11.5
201942_s_at	D8S390.1	FLJ3409	0.6	1.7	0.6	1.3	1.7	1.6	7.0	2.4	2.6	15.9	23.8	6.8	81	0.5	0.8	1.3	2.5
220933_S_at	NM_024617.1	glycerol-3-phosphate dehydrogenase	2.1	2.0	9.6	14.2	14.0	7.1	7.2	10.9	12.5	38.1	37.3	81.5	57.8	1.9	3.1	4.8	6.2
221764_at	AL574186	Toll-like receptor 6	6.3	4.4	16.5	18.6	15.0	10.4	15.8	21.9	22.7	80.9	99.2	46.3	60.3	9.5	89	9.4	57
207446_at	NM_006068.1	chromosome 6 open reading frame 76	0.5	0.5	0.7	1.5	0.8	0.8	0.9	1.2	0.8	7.6	11.8	7.2	8.7	0.7	0.9	0.9	1.2
219748_at	NM_024807.1		0.2	0.3	0.3	0.4	0.6	1.9	2.6	1.6	1.6	9.1	9.1	6.7	6.4	0.2	0.3	0.6	1.1
220945_s_at	NM_018050.1	FLJ10298	1.0	1.4	0.5	0.7	0.7	1.1	0.6	1.5	1.0	8.0	10.8	13.6	11.0	1.1	0.5	0.3	0.6
212577_X_at	AA68554	KIAA0650	1.9	1.3	6.4	8.0	9.9	10.1	24.0	8.1	9.4	74.0	98.6	42.2	57.4	4.4	10.8	9.5	4057
221732_at	AK026161.1	RIKEN cDNA S830420C20 apoptosis-associated tyrosine kinase	2.8	0.7	3.4	10.5	8.8	5.0	6.0	10.7	10.9	27.6	31.6	30.8	34.7	0.3	0.4	1.8	2.5
203985_at	NM_004920.1	acyl-Coenzyme A oxidase 1, palmitoyl- α , β -hydrolase	1.6	1.3	0.7	1.0	0.5	0.3	0.3	1.4	1.0	10.5	15.8	13.3	15.2	3.2	1.0	0.5	0.4
213501_at	T62995	stearoyltransferase (STHM)	1.3	1.1	2.0	2.6	2.8	1.3	0.9	1.2	0.6	85	11.5	12.4	12.5	0.1	1.1	0.3	1.4
204542_at	NM_005456.1		0.4	0.2	1.5	0.3	0.2	3.4	3.9	4.5	32	13.0	13.4	21.0	13.4	0.7	0.7	0.3	0.6

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Fig. 6G

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C. Neutrophil (Ne)-selective transcripts (5/7).

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C. Neutrophil (Ne)-selective transcripts (6/7).

Probe set	Accession #	Transcripts	MC card	MC blood	MC lung	Ba1 (small)	Ba2 (small)	Eo (small)	Eo3 (small)	Eo4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ne5L		
207072_at	NM_003053.1	Interleukin 18 receptor accessory protein ([IL18RAP])	5.9	0.9	22	3.4	4.1	7.2	1.6	2.8	1.7	134	9.7	20.9	5.6	24	2.8	3.1	0.4	1.6	0.3	35722	
215719_X_at	X83493.1	R	1.0	0.6	3.1	2.7	1.6	2.2	5.2	1.8	1.7	190	31.9	11.4	9.4	1.0	4.5	2.2	1.6	1.1	4.4	35557	
218404_at	NM_013322.1	sorting nexin 10 phosphatidylycerophosphate synthase [GS1]	4.9	1.2	2.6	5.0	3.7	0.7	0.1	2.1	0.7	285	31.8	34.8	33.8	0.3	12	1.9	9.0	6.5	0.3	3563	
219394_at	NM_024419.1	KIAA0690	3.4	3.0	1.7	4.2	3.5	2.4	3.8	6.1	9.2	172	16.9	17.5	16.3	1.0	2.1	2.6	2.4	1.5	1.7	35554	
216913_s_at	AK01160.1	GPR	0.1	0.3	0.1	0.1	0.1	1.9	2.5	2.3	2.8	8.9	8.3	7.5	10.9	0.1	0.1	0.2	2.5	0.1	0.0	35402	
205118_at	M60261	formylpeptidase receptor 1	0.1	0.2	0.8	0.1	1.1	0.1	0.4	0.6	0.1	3.9	3.2	7.8	2.1	0.1	0.1	1.4	0.1	0.0	35295		
210564_X_at	AF09619.1	FLAME-1-delta	1.4	1.5	5.3	6.6	7.0	4.3	4.2	5.9	3.5	212	30.3	18.4	19.6	2.1	2.9	4.0	4.6	3.0	1.8	35148	
213607_X_at	BE551347	KIAA0134	1.3	1.3	2.9	2.0	1.7	8.7	15.8	3.5	4.3	42.7	42.5	11.1	15.3	0.6	1.3	1.9	6.2	1.7	0.9	3514	
203888_at	NM_000361.1	thrombomodulin	0.9	0.6	0.1	0.1	0.3	0.2	0.4	0.8	0.1	6.1	6.4	4.6	0.2	0.3	0.1	0.1	0.6	0.5	0.1	35126	
210233_at	AF167343.1	interleukin 1 receptor accessory protein ([IL1RAp])	0.5	0.1	0.0	0.1	0.6	0.8	0.4	0.6	0.7	1.8	3.0	2.0	2.3	0.6	0.0	0.0	0.0	0.0	0.3	35023	
204959_at	NM_002432.1	myeloid cell nuclear differentiation antigen	1.2	0.6	24.2	50.0	26.2	17.5	17.9	49.8	22.3	249.8	290.2	186.0	217.0	3.4	1.6	0.6	66.6	25	0.0	34903	
217967_s_at	AF288991.1	riban	6.3	3.7	16.3	42.4	33.9	27.9	29.5	43.0	30.9	107.4	115.3	117.9	110.3	2.6	7.5	9.9	4.9	3.4	20.4	34847	
221763_s_at	A1694023	thyroid hormone receptor interactor 8 leucocyte immunoglobulin-like receptor, subfamily A (with TM domain) member 2 ([LRRA2])	0.8	1.5	1.9	4.6	5.5	5.5	6.9	9.9	9.0	28.3	32.9	34.0	42.7	1.1	3.7	4.1	5.1	9.8	3.0	34777	
207857_at	NM_006866.1	R	0.4	0.5	3.6	8.5	5.3	4.5	4.9	1.6	6.3	33.5	34.3	46.2	50.8	1.8	0.0	0.1	11.6	0.5	0.1	34773	
220740_s_at	NM_005135.1	solute carrier family 12 member 6 [SLC12A6]	1.6	1.0	2.5	3.3	3.4	3.5	5.6	3.2	3.2	126	190	107	14.4	4.0	2.9	2.2	2.9	3.5	0.8	34722	
217739_s_at	NM_005746.1	pie-3-cell colony-enhancing factor	7.1	1.7	9.9	46.0	61.0	189	13.9	12.9	9.3	112.4	120.5	90.8	93.4	1.2	2.3	1.4	17.6	2.1	3.1	34242	
205041_s_at	NM_009097.1	prosomere 1 (CRM1)	0.3	1.0	0.4	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0.1	0.1	0.5	0.0	0.0	34189	
214784_X_at	BE562.99	exportin 6	7.4	5.0	10.0	23.7	23.9	13.0	16.7	23.3	20.5	60.3	67.8	57.2	60.8	2.9	8.7	7.8	6.6	5.9	5.4	34155	
217985_s_at	AA102574	bromodomain adjacent to zinc finger domain 1A [KIAA0933]	1.5	1.4	1.8	2.6	3.8	7.4	5.1	7.3	4.7	16.9	192	22.1	24.2	2.7	2.5	2.3	3.5	2.4	0.9	33999	
219053_s_at	A1806395	FLJ20847	0.1	0.7	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	5.5	7.3	3.1	3.2	0.2	0.1	0.0	1.0	1.3	33933	
217475_s_at	NM_017966.1	PA6 clone IP3-515N1	0.6	0.5	0.6	0.2	0.4	1.3	0.5	0.5	0.5	12	5.9	9.8	1.6	1.4	0.7	0.3	0.1	0.5	0.7	0.2	33448
463323_at	AL120741	Ca2+-dependent endoplasmic reticulum nucleoside diphosphatase [KIAA0625]	4.4	3.2	42	83	72	53	6.7	11.4	7.9	20.0	21.5	33.9	26.3	2.5	2.8	3.6	4.3	3.4	5.0	33038	
201965_s_at	NM_015046.1	insulin-like growth factor 1 receptor [IGFR]	2.7	3.1	3.3	8.5	8.3	4.9	5.8	7.4	7.5	19.5	18.5	18.7	22.8	2.2	3.4	4.6	5.6	5.6	2.6	33019	
203828_at	NM_0008752	R	0.5	0.1	3.7	3.0	4.0	6.8	4.9	2.7	5.8	18.8	23.4	6.8	20.6	1.6	0.1	2.8	2.4	2.0	3.5	32989	
202193_at	NM_0055692	LM domain kinase 2 [LMK2] transcript variant 2a	1.8	1.5	1.9	5.6	5.6	6.4	4.8	11.3	8.9	17.0	20.5	36.5	28.2	0.1	1.3	1.1	0.6	0.5	0.8	32887	
203042_at	NM_002294.1	lysosomal-associated membrane protein 2 [LAMP2]	2.4	3.1	1.1	1.7	1.3	5.9	6.4	12.4	10.7	21.3	27.0	44.1	35.4	0.8	0.6	0.5	3.2	0.8	0.4	32536	
220326_s_at	NM_018071.1	FLJ10357	5.1	4.5	1.9	1.2	1.9	6.3	8.9	5.2	8.5	25.3	28.1	19.2	21.0	0.9	0.1	0.7	6.4	0.1	4.7	32404	
212470_s_at	AB011088.1	spem-associated antigen 9	4.0	2.9	3.3	6.3	7.2	4.5	4.0	4.7	4.9	13.2	17.0	18.1	24.0	1.2	2.5	2.2	3.9	3.0	5.4	32282	
211133_X_at	AF09843.1	clone 6 immunoglobulin-like transcript 5	1.9	1.4	0.8	1.5	1.3	3.1	2.7	3.8	2.1	42.1	42.2	27.0	25.1	2.7	0.9	0.5	10.2	0.4	0.2	32288	
219313_at	NM_017577.1	DKFZp4340328	0.0	0.8	0.2	0.0	0.4	0.2	0.1	0.1	0.0	38.8	33.7	3.1	5.6	0.2	0.1	0.1	1.2	0.1	0.1	32759	
221149_at	NM_018485.1	GPR	0.2	0.1	0.8	0.7	1.2	0.7	0.9	0.9	0.6	33	32	4.2	2.9	0.0	0.3	0.2	1.0	0.1	0.3	32688	
203433_at	NM_006441.1	5,10-methylenefattyhydrofolate synthetase	1.4	1.8	1.5	2.5	1.6	3.1	4.2	3.5	3.1	15.8	11.4	9.6	9.0	1.6	1.8	1.9	2.9	1.7	1.5	32181	
214486_X_at	AF041459.1	FADD-like apoptosis regulator	1.9	2.1	10.7	5.0	6.5	4.2	5.3	4.3	6.0	26.3	16.2	25.3	24.2	2.4	3.7	5.0	5.3	2.3	1.9	32114	

Fig. 61

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C. Neutrophil (Ne) selective transcripts (7/7).

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba 1 (small)	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2 (small)	Eo 3 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ba 5L		
203222_s_at	BC002961_AA87765	oxysterol binding protein-like 2 ubiquitin-conjugating enzyme/E2B mitogen-activated protein kinase kinase 4 FLJ0357	1.3 3.3	0.2 3.4	2.7 4.8	8.8 15.5	8.0 5.3	5.4 7.2	7.7 14.7	7.3 12.8	17.2 20.9	18.4 25.6	22.3 43.6	23.9 38.1	0.9 4.0	23 45	3.4 3.9	28 39	20 45	13 46	3.1877 3.1877		
203334_s_at	NM_003010.1_R2449	LM domain kinase 2 Elys transcription factor-like protein TMIS62 TRAF and TNF receptor-associated protein (ADAM22) BRAF35/ADA2 complex (80 kDa) transmembrane gamma-carboxyglutamic acid Dicer 4	3.7 4.5	2.4 5.4	4.9 15	8.2 3.9	6.3 3.0	2.5 9.6	4.8 12.8	6.8 16.4	14.7 28.0	15.2 27.6	27.4 46.7	26.9 44.1	2.8 12	24 0.6	26 0.1	27 6.5	23 0.1	27 0.2	3.1804 3.1803		
203266_s_at	AL11466.1	LM domain kinase 2 Elys transcription factor-like protein TMIS62 TRAF and TNF receptor-associated protein (ADAM22) BRAF35/ADA2 complex (80 kDa) transmembrane	3.8	1.9	4.3	5.1	4.8	8.7	10.3	10.8	9.4	33.9	36.5	30.8	23.8	1.3	1.7	1.8	1.9	0.9	1.4	3.1609	
214766_s_at	AL080144.1	1.3 2.1	0.2 2.8	2.0 2.7	3.1 4.8	4.2 11.0	1.9 5.7	1.4 5.0	2.1 7.4	2.4 14.0	9.5 36.1	9.9 16.6	64.5 31.0	57.5 30.6	4.5 0.1	7.7 3.0	9.4 4.5	5.3 3.1	8.2 2.7	6.3 3.0	3.1414 3.1402 3.1382		
203266_s_at	NM_016614.1	gamma-carboxyglutamic acid Dicer 1, Dcr-1 homolog (Drosophila) solute carrier family 31 ornithine decarboxylase antizyme clone 1,6 immunoglobulin-like transcript v-yes-1 farnacuchi/sarcoma viral related oncogene homolog (LYN) hypothetical protein NM_0076706 major histocompatibility complex, class I, B retinitis pigmentosa GTPase regulator interacting protein 1 (RPGRIP1)	0.1 0.5	1.2 1.7	1.3 1.3	1.4 0.3	1.1 0.8	0.9 1.7	0.2 0.9	0.2 2.3	0.4 2.3	0.4 2.2	0.4 2.1	0.4 2.1	0.2 5.1	3.8 27.7	0.2 22	0.2 5.1	0.1 6.3	1.9 12.2	1.1 6.2	0.4 6.2	3.1336 3.1326 3.1262 3.1253
207291_s_at	NM_024081.1_B550131	v-yes-1 farnacuchi/sarcoma viral related oncogene homolog (LYN) hypothetical protein NM_0076706 major histocompatibility complex, class I, B retinitis pigmentosa GTPase regulator interacting protein 1 (RPGRIP1)	0.1 0.5	1.2 1.7	1.3 1.3	1.4 0.3	1.1 0.8	0.9 1.7	0.2 0.9	0.2 2.3	0.4 2.2	0.4 2.1	0.4 2.1	0.4 2.1	0.2 5.1	3.8 27.7	0.2 22	0.2 5.1	0.1 6.3	1.9 12.2	1.1 6.2	0.4 6.2	3.1336 3.1326 3.1262 3.1253
213220_s_at	NM_001860.1_AF24221.1	1.4 2.1	0.1 1.2	2.1 2.4	2.1 2.5	2.2 2.2	2.8 2.1	5.1 5.1	4.8 5.1	4.8 14.8	4.8 12.0	4.8 12.0	31.8 24.6	36.3 19.2	0.2 2.0	0.2 2.4	0.2 2.1	0.9 5.2	17.1 2.1	23.6 7.5	0.5 1.6	3.1131 3.1131	
204204_s_at	NM_003642_AW49184	1.4 2.1	0.1 1.2	2.1 2.4	2.1 2.5	2.2 2.2	2.8 2.1	5.1 5.1	4.8 5.1	4.8 14.8	4.8 12.0	4.8 12.0	31.8 24.6	36.3 19.2	0.2 2.0	0.2 2.4	0.2 2.1	0.9 5.2	17.1 2.1	23.6 7.5	0.5 1.6	3.1131 3.1131	
210784_X_at	AF006344.1	2.5 3.0	3.0 3.4	3.8 3.8	3.8 6.7	6.6 6.6	7.6 7.6	6.6 6.6	25.2 25.2	17.9 17.9	21.3 21.3	29.4 29.4	26 25	25 25	2.4 2.4	2.5 2.5	2.5 2.5	7.4 7.4	1.8 1.8	2.8 2.8	3.0985		
206295_s_at	AI336412	1.1 1.4	1.4 0.1	1.2 2.1	1.2 2.4	2.5 2.5	2.2 2.2	2.8 2.1	5.1 5.1	4.8 14.8	4.8 12.0	4.8 12.0	31.8 24.6	36.3 19.2	0.2 0.2	0.2 0.2	0.2 0.2	13.3 2.1	0.3 5.2	0.2 1.6	0.2 3.1	3.1236	
221895_s_at	AW49184	2.5 3.0	3.0 3.4	3.8 3.8	3.8 6.7	6.6 6.6	7.6 7.6	6.6 6.6	25.2 25.2	17.9 17.9	21.3 21.3	29.4 29.4	26 25	25 25	2.4 2.4	2.5 2.5	2.5 2.5	7.4 7.4	1.8 1.8	2.8 2.8	3.0985		
37384_s_at	D13640	1.1 1.8	1.4 0.1	1.2 2.1	0.8 8.2	1.0 7.6	1.1 2.8	1.0 0.4	1.0 0.4	0.5 0.8	1.4 1.4	6.1 5.9	34.4 88.0	53 94.4	4.7 99.8	1.5 1.6	0.9 1.3	0.8 1.3	1.3 0.1	0.7 26.3	0.4 0.9	0.4 0.4	3.0985
206608_s_at	NM_020366.1	1.1 1.8	1.4 0.1	1.2 2.1	0.8 8.2	1.0 7.6	1.1 2.8	1.0 0.4	0.5 0.8	1.4 1.4	6.1 5.9	34.4 88.0	53 94.4	4.7 99.8	1.5 1.6	0.9 1.3	0.8 1.3	1.3 0.1	0.7 26.3	0.4 0.9	0.4 0.4	3.0985	
204924_s_at	NM_003364.1	2.0 2.0	2.0 2.0	2.0 2.0	0.7 0.7	0.7 0.7	22.0 22.0	29.1 29.1	0.3 0.3	5.2 5.2	0.3 0.3	0.3 0.3	0.3 0.3	0.3 0.3	0.3 0.3	3.0985							
204781_s_at	NM_000443.1	2.0 2.0	2.0 2.0	2.0 2.0	0.7 0.7	0.7 0.7	22.0 22.0	29.1 29.1	0.3 0.3	5.2 5.2	0.3 0.3	0.3 0.3	0.3 0.3	0.3 0.3	0.3 0.3	3.0985							
203405_s_at	AI806395	2.0 2.1	2.0 1.7	2.0 3.0	0.7 0.7	0.7 0.7	22.0 22.0	29.1 29.1	0.3 0.3	5.2 5.2	0.3 0.3	0.3 0.3	0.3 0.3	0.3 0.3	0.3 0.3	3.0985							
203405_s_at	AF006161	2.0 2.1	2.0 1.7	2.0 3.0	0.7 0.7	0.7 0.7	22.0 22.0	29.1 29.1	0.3 0.3	5.2 5.2	0.3 0.3	0.3 0.3	0.3 0.3	0.3 0.3	0.3 0.3	3.0985							
203405_s_at	NM_00448.1	2.0 2.1	2.0 1.7	2.0 3.0	0.7 0.7	0.7 0.7	22.0 22.0	29.1 29.1	0.3 0.3	5.2 5.2	0.3 0.3	0.3 0.3	0.3 0.3	0.3 0.3	0.3 0.3	3.0985							
204949_s_at	NM_0021622	3.0 3.7	3.7 0.3	5.7 0.2	4.63 0.1	34.5 0.1	38.9 0.1	51.6 0.7	94.5 1.0	93.7 10.0	16.1 10.0	168.3 143	239.1 250	241.1 250	4.5 2.1	13.6 1.2	21.0 0.1	17.6 0.1	19.9 0.1	1.3 0.1	3.0617 3.0617		
205208_s_at	NM_000717.2	3.0 3.7	3.7 0.3	5.7 0.2	4.63 0.1	34.5 0.1	38.9 0.1	51.6 0.7	94.5 1.0	93.7 10.0	16.1 10.0	168.3 143	239.1 250	241.1 250	4.5 2.1	13.6 1.2	21.0 0.1	17.6 0.1	19.9 0.1	1.3 0.1	3.0617 3.0617		
213727_s_at	AI74554	2.1 2.1	2.1 1.7	3.0 3.0	15.0 15.0	12.1 12.1	8.9 8.9	13.7 13.7	25.4 25.4	23.9 23.9	49.9 49.9	28.3 28.3	59.9 59.9	75.8 75.8	0.7 0.7	4.5 4.5	6.6 6.6	5.7 5.7	5.4 5.4	3.7 3.7	3.0554		
202626_s_at	NM_002350.1	1.55 1.1	9.5 0.3	12.1 0.2	12.7 0.4	14.8 0.7	32.6 1.0	31.6 1.2	54.0 54.0	41.0 41.0	110.1 110.1	115.1 115.1	122.7 122.7	127.2 127.2	18.4 18.4	2.1 3.0	36.8 33.3	33.0 1.4	33.0 0.4	33.0 0.4	33.0 0.3	3.0541	
208420_s_at	NM_005849.1	1.1 21.4	0.3 17.4	0.2 4.6	0.4 24.8	0.7 20.1	13.3 13.3	19.5 19.0	33.9 27.3	25.7 25.7	60.4 60.4	58.2 58.2	89.2 89.2	86.2 86.2	2.2 2.2	6.6 6.6	11.3 11.3	12.8 12.8	7.6 7.6	7.3 7.3	3.0391		
206151_s_at	NM_007229.1	2.0 2.0	1.0 1.0	1.3 1.3	3.7 3.6	2.0 2.0	1.5 1.5	4.4 4.4	3.7 3.7	6.7 6.7	6.9 6.9	9.2 9.2	9.9 9.9	1.0 1.0	2.1 2.1	1.3 1.3	1.3 1.3	1.0 1.0	1.6 1.6	0.1 0.1	3.0361		
219540_s_at	AU150728	1.4 6.0	1.2 5.4	2.8 12.4	3.7 32.8	3.7 33.1	14.9 14.9	19.0 19.0	27.3 27.3	25.7 25.7	60.4 60.4	58.2 58.2	89.2 89.2	86.2 86.2	2.2 2.2	6.6 6.6	11.3 11.3	12.8 12.8	7.6 7.6	7.3 7.3	3.0329		
203265_s_at	AA810268	1.4 2.0	1.2 1.0	2.8 2.1	4.5 3.7	1.7 2.0	2.6 1.5	4.4 4.4	3.5 3.5	3.1 3.1	12.8 12.8	10.4 10.4	16.8 16.8	1.4 1.4	1.3 1.3	1.3 1.3	1.3 1.3	1.0 1.0	2.5 2.5	1.5 1.5	3.028		
203030_s_at	AF007555.1	0.9 0.7	0.0 1.0	1.6 0.8	1.2 1.9	0.1 2.6	0.1 30	0.1 8.4	0.1 8.4	0.1 8.4	0.1 8.4	0.1 8.4	0.1 4.9	0.1 37.3	0.1 24.4	0.1 27.0	0.1 1.2	0.1 4.6	0.1 5.3	0.1 5.3	0.1 5.3	3.0269	
203730_s_at	NM_005526.1	2.0 2.0	3.0 1.0	4.9 0.8	6.0 0.6	3.5 2.2	4.3 2.1	12.4 14.4	4.4 4.4	3.0 2.1	24.2 13.8	27.0 24.7	15.4 15.4	12.0 12.0	0.3 0.5	1.8 1.0	1.2 0.5	6.2 0.9	6.2 1.0	0.5 0.5	3.0143 3.0112		
204747_s_at	NM_001549.1	2.0 0.7	3.0 1.0	4.9 0.8	6.0 0.6	3.5 2.2	4.3 2.1	12.4 14.4	4.4 4.4	3.0 2.1	24.2 13.8	27.0 24.7	15.4 15.4	12.0 12.0	0.3 0.5	1.8 1.0	1.2 0.5	6.2 0.9	6.2 1.0	0.5 0.5	3.0143 3.0112		

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Fig. 6J

D. Mast cell (MC)-selective transcripts (1/2).

ProbeSet	Accession #	Transcripts	MC cond blood	MC lung	Ba 1 (small)	MC	Ba 2	Ba 3	Eo	Fo	Eo 3	Eo 4	Ne	Ne 3	Ne 4	Ne 5	CD4 (small) 1	CD4 (small) 2	CD8 (small) 1	CD8 (small) 2	CD14 (small) 1	CD14 (small) 2	CD19	Fb	MCSL					
217032_X_at	AF09143	tryptase beta	1694	118.7	0.7	1.1	0.4	0.1	0.1	0.5	0.1	0.2	0.1	0.5	0.4	0.3	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	202148				
215382_X_at	AF206566	tryptase beta	1681	108.4	1.7	0.7	0.4	0.2	0.2	0.2	0.1	0.1	0.3	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	172668			
204041_at	NM_000898	monooamine oxidase B	235	46.9	0.2	0.7	0.1	0.1	0.2	0.6	0.3	0.1	0.2	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	136311		
210984_X_at	AF206565	tryptase epsilon	131.1	92.3	0.7	1.2	0.2	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	112376		
216474_X_at	AF206567	tryptase beta	2100	120.9	2.4	2.0	1.4	1.2	0.4	0.2	0.1	0.2	1.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	843375		
205583_X_at	NM_0032942	tryptase beta	1955	95.3	2.4	2.7	0.3	0.2	0.2	0.6	0.6	0.4	0.1	0.4	1.0	2.0	0.7	0.2	0.3	0.2	0.1	0.1	0.1	0.1	0.1	0.1	0.1	672617		
207741_X_at	NM_0032932	tryptase alpha	1750	99.7	2.2	2.2	1.8	0.5	0.2	0.3	0.2	0.2	0.2	0.3	0.3	0.2	0.1	0.5	0.3	0.2	0.1	0.1	0.1	0.1	0.1	0.1	0.1	59015		
207134_X_at	NM_0241642	tryptase beta	2146	112.3	3.1	3.8	1.7	1.2	0.3	0.8	0.4	0.6	0.3	0.8	0.4	0.6	0.5	0.2	1.1	0.4	0.6	0.1	0.1	0.1	0.1	0.1	0.1	0.1	571834	
205563_at	NM_0019111	cathepsin G	912	57.0	2.7	1.1	0.9	0.4	0.3	0.1	0.1	0.1	0.1	0.1	1.4	1.6	0.7	0.7	0.2	0.4	1.3	0.3	0.1	0.1	0.1	0.1	0.1	0.1	514749	
205266_at	NM_0023092	leukemia inhibitory factor	170	9.8	0.2	0.2	0.3	0.1	0.2	0.2	0.1	0.1	0.1	0.2	0.1	0.4	0.7	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	443659	
210324_at	NM_177631	complement protein C8 gamma	29	6.9	0.1	0.1	0.0	0.0	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	33806	
211743_s_at	BC005929	major basic protein	743	70.7	1.0	4.7	2.7	0.1	0.7	0.8	0.6	0.2	0.3	0.7	0.2	0.1	0.2	0.2	0.3	0.2	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	315559	
211549_s_at	U632961	15-hydroxyprostaglandin dehydrogenase	483	48.3	2.1	2.5	1.4	1.5	1.3	0.8	0.9	0.1	0.1	0.2	0.2	0.1	0.1	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	248454			
206726_at	NM_014485	prostaglandin D2 synthase	1190	90.0	5.0	7.8	5.7	0.7	0.1	0.0	0.5	0.2	0.2	0.2	0.6	0.1	0.3	1.2	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	17432		
205011_at	NM_014622	loss of heterozygosity, 11, chromosomal region 2, gene A	76.1	70.9	3.0	6.8	4.5	2.3	1.0	1.4	1.9	0.2	1.1	1.2	1.8	2.9	2.2	1.3	1.7	2.0	2.6	162511								
205428_s_at	NM_0017402	calbindin 2	16.7	63.4	1.3	0.7	0.9	0.4	1.6	0.7	1.3	1.8	1.6	1.6	1.6	1.6	1.7	1.7	1.3	0.6	0.9	161621								
219255_at	NM_024554	FJ11413 tyrosine kinase with immunoglobulin and epidermal growth factor homology domains	100	92.1	0.1	0.1	0.1	0.2	0.1	0.6	0.1	0.6	0.1	0.6	0.1	0.6	0.1	0.6	0.1	0.6	0.1	0.6	0.1	0.6	0.1	0.6	0.1	0.6	0.1	15339
204468_s_at	NM_0035424	CP7A promoter binding factor	3.6	23.8	0.5	0.3	0.1	0.0	0.1	0.2	0.0	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.1	0.1	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	144259	
208343_s_at	AF46343	CD117 c-KIT	1.5	0.9	0.0	0.0	0.3	0.1	0.0	0.1	0.1	0.1	0.0	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	138025	
205051_s_at	NM_0002221	R	92.1	85.8	62	81	73	23	52	65	27	0.7	21	28	1.1	0.8	0.2	0.5	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	123815		
210102_at	BC001234	chromosomal region 2, gene A	40.9	41.1	2.8	3.7	4.5	0.3	0.4	0.3	0.6	0.7	0.9	0.2	0.6	1.8	0.8	0.7	1.2	0.6	1.3	113619								
210796_X_at	D863591	stomatobinding Ig-like lectin, siglec6	17.8	26.0	1.5	1.0	1.1	1.2	1.5	1.3	1.4	1.4	2.3	1.7	1.3	2.0	1.4	1.5	1.8	1.0	0.8	105398								
206519_X_at	D863581	static acid binding Ig-like lectin, siglec6	88	16.0	0.3	0.3	0.4	0.0	0.0	0.0	0.1	0.0	0.1	0.1	0.1	0.1	0.5	0.2	0.5	0.0	0.0	0.4	0.0	0.0	0.4	0.0	0.4	0.0	10.13	
206480_at	NM_000897	leukotriene C4 synthase	10.6	6.2	1.2	0.1	0.4	2.4	1.6	0.5	0.1	0.2	1.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	927381	
206617_s_at	NM_0029104	tudor domain containing 3	6.0	13.4	0.8	0.6	0.2	0.5	0.7	0.5	0.5	0.1	0.6	0.6	0.3	0.0	0.7	0.7	0.3	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	918229	
208089_s_at	NM_030794	ADAMTS3 disintegrin-like and metalloprotease (reptilase type 1 motif)	18.1	7.2	0.1	0.4	0.7	0.1	0.3	0.2	0.4	0.1	0.4	0.1	0.8	0.4	0.1	0.8	0.1	0.2	0.1	0.8	0.1	0.1	0.1	0.8	0.1	0.1	816897	
205466_s_at	NM_005114	thrombospondin type 1 motif, 3 tissue-plasminogen activator	6.8	4.3	0.5	0.7	0.8	0.5	0.7	0.6	0.4	0.5	0.4	0.7	0.7	1.2	0.7	0.6	0.4	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	72214	
214913_at	AB002264	siglec6	222	29.7	0.2	0.4	0.1	0.1	0.3	0.5	0.5	0.1	0.1	0.1	0.1	0.1	1.3	0.4	1.6	0.1	0.2	0.6	0.1	0.1	0.1	0.1	0.1	0.1	0.1	570228
201880_s_at	NM_000930	L18B protein	190	22.7	2.4	1.1	0.8	1.1	1.5	1.3	1.0	2.0	2.0	0.4	1.4	2.9	2.1	2.3	1.9	1.2	1.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	510738
220532_s_at	NM_014020	FJ10305	524	18.2	0.8	0.8	1.0	6.4	2.9	1.5	1.2	0.4	0.3	1.4	0.6	2.2	0.6	2.2	5.0	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	61662		
218169_at	NM_018052	nuclear receptor subfamily 1, group 1, member 3 tudor domain containing 3	6.2	14.6	0.3	0.2	0.4	0.4	0.3	0.3	0.4	0.6	0.5	0.1	0.1	0.5	1.6	0.3	1.6	0.3	1.0	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	604597
221728_X_at	AK025198		5.6	5.5	0.6	0.9	1.0	0.4	3.6	0.9	0.8	0.7	0.6	1.4	0.9	0.9	0.8	0.7	0.7	0.7	0.8	0.7	0.7	0.7	0.7	0.7	0.7	0.7	5.70228	
214028_X_at	AU158998		3.2	11.9	0.9	0.9	0.4	0.8	0.3	0.4	0.7	0.6	0.6	0.1	0.1	0.8	1.2	1.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	510738	
221552_at	BC001698		10.6	3.4	0.9	1.8	1.1	0.9	1.1	1.0	0.9	0.2	0.2	0.7	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	502434	
203367_at	NM_007026		15.0	45.4	1.2	0.9	0.8	0.9	0.9	0.8	0.1	0.2	0.7	0.4	0.3	0.4	0.3	0.7	0.3	0.2	0.6	0.3	0.2	0.6	0.3	0.2	0.6	0.2	481127	
206597_s_at	NM_004807		4.2	3.8	0.2	0.1	0.1	0.4	0.4	0.1	0.1	0.3	0.4	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1

Fig. 6K

D. Mast cell (MC)-selective transcripts (2/2).

Probe set	Accession #	Transcripts	MC cord	MC blood	MC lung	MC Ba 1 (small)	MC Ba 2	MC Ba 3	MC Eo	MC Eo3	MC Eo4	MC Ne	MC Ne3	MC Ne4	pl	CD4	CD8	CD14	CD19	Fb	MCSL1
207480_s_at	NM_020149.1	TALE homeobox protein Meis2e	14.0	14.9	1.9	3.6	4.0	17	19	5.3	3.8	0.3	0.6	1.0	0.3	0.5	0.8	0.4	0.6	0.4	0.8
452882_at	AA209239	lipase	10.9	3.0	0.2	2.1	0.8	0.5	0.5	1.3	0.9	0.1	0.1	0.2	0.1	0.4	0.5	0.5	1.3	1.0	0.9
207039_at	NM_000077.1	Cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	7.5	3.6	0.7	0.7	0.1	0.6	0.4	0.3	0.5	0.1	1.2	0.6	1.1	0.1	0.9	0.5	0.8	0.1	1.2
201650_at	NM_002276.1	keratin 19	62	120	0.0	0.0	0.3	0.1	0.0	0.0	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.0	20.453547
214533_at	NM_001856.1	chymase	10.1	27	0.4	0.2	0.8	0.1	0.1	0.8	0.6	0.1	0.1	0.2	0.2	1.2	0.7	0.5	1.0	0.4	0.3
218211_s_at	NM_024101.1	melanophillin	24.8	29.6	2.7	2.5	1.8	3.0	2.5	1.9	2.2	4.6	4.1	3.3	4.1	6.4	4.0	3.2	24	3.4	27
203916_at	NM_003635.1	N-deacetylase/N-sulfotransferase	17.9	26.7	3.2	6.5	6.8	2.5	2.7	3.6	3.1	4.2	3.4	5.5	5.2	0.9	3.1	4.9	3.3	2.7	24
212336_at	AB022336.1	erythrocyte membrane protein band 4.1-like 1	3.8	6.4	0.1	0.2	0.1	0.5	0.1	0.2	0.4	0.1	0.1	0.1	0.5	0.1	0.4	0.2	0.4	0.4	0.4
200766_at	NM_001969.1	cathepsin D	42.6	39.5	2.5	5.3	4.3	4.8	3.4	2.7	4.0	6.7	3.1	1.9	2.6	1.6	2.5	10.0	1.6	5.9	41.037
202218_s_at	NM_004265.1	delta-6 fatty acid desaturase (FADS6)	18.8	24.5	0.4	0.2	1.0	0.3	0.1	0.8	0.5	0.2	0.1	0.1	0.1	0.1	0.6	0.1	0.1	0.6	0.5
204066_s_at	NM_014914.1	centaurin gamma 2	53	79	0.4	0.4	0.7	0.2	0.2	0.6	0.6	0.3	0.5	0.4	0.4	0.8	0.6	1.6	0.6	1.0	16.405648
209644_X_at	U38945.1	Cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	14.0	6.4	1.0	1.4	0.7	1.2	1.3	1.7	1.5	1.0	1.6	1.5	2.1	2.3	1.8	1.5	0.9	0.3	2.4
221679_s_at	AF22418.1	lipase	2.8	1.9	0.4	0.9	0.1	0.3	0.4	0.4	0.1	0.1	0.5	0.0	0.5	0.5	0.1	0.6	0.5	0.2	12.412758
211538_s_at	U56725.1	heat shock protein 70kD	44	74	0.3	0.6	0.4	0.6	0.3	0.3	0.9	1.4	0.4	1.0	0.8	1.5	0.5	0.1	0.5	0.7	3.884549
211548_s_at	J05594.1	15-hydroxyprostaglandin dehydrogenase nuclear receptor subfamily 5, group A member 2	82.6	60.0	19.4	26.0	16.3	32	29	1.8	1.7	0.8	0.5	0.9	0.2	4.1	12	0.9	0.1	0.6	0.2
210174_at	AF228413.1	RAB38, member RAS oncogene	2.9	3.4	0.5	0.5	0.6	0.8	1.1	0.7	1.2	1.1	0.4	0.1	0.4	0.9	0.7	0.2	0.2	0.6	0.3
219412_at	NM_022337.1	gelatin-like capping protein (actin filament)	3.9	4.0	0.1	0.4	0.3	0.7	0.1	0.2	0.3	0.2	0.2	1.1	0.1	1.2	0.1	0.8	0.4	0.1	0.5
201850_at	NM_001747.1	KIAA0555	70.5	64.5	9.6	30.8	28.8	8.1	7.8	11.5	9.9	26	3.6	3.0	2.4	1.6	1.1	1.0	17.0	5.8	5.3
205888_s_at	AI92693	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	5.4	4.6	0.7	1.6	1.2	0.8	0.7	0.1	1.0	1.3	0.3	0.2	0.6	1.2	0.3	1.5	0.7	1.2	0.4
221750_at	BG035985	nuclear receptor subfamily 1, group I, member 3	5.0	3.8	0.9	1.5	1.1	1.1	1.2	1.3	1.0	1.3	0.5	0.7	1.2	0.7	0.5	1.1	0.7	1.4	1.2
214248_s_at	AV693347	FLJ21080	35	3.5	0.7	0.6	0.7	0.5	2.2	0.5	0.7	1.2	0.6	0.1	1.1	0.9	0.3	0.6	0.8	0.4	
218788_s_at	NM_022743.1	SH3-domain protein 5 (ponsin)	16.1	23.7	0.5	2.5	0.9	1.1	2.7	2.1	1.1	0.8	0.8	0.9	2.3	2.1	2.9	0.6	2.0	6.3	3.07851
218087_s_at	NM_013385.1	prostate differentiation factor	1.4	1.9	0.4	0.9	0.4	0.5	0.0	0.0	0.1	0.0	0.1	0.0	0.2	0.1	0.0	0.2	0.2	0.1	3.07366
221577_X_at	AF083934.1	GM2 activator protein	7.8	5.5	0.6	0.3	0.5	0.6	0.1	0.2	0.6	0.0	0.2	0.3	0.1	0.1	0.2	0.0	0.1	0.4	2.1
35820_at	X62078	heat shock 10kD	21.8	17.6	1.4	3.3	1.3	0.3	0.3	0.2	0.5	0.8	1.9	0.3	0.4	0.2	0.2	0.2	6.5	5.0	2.7
208744_X_at	BG433660		7.3	4.8	0.5	0.2	0.2	0.9	0.1	0.4	0.6	0.1	0.1	0.4	0.1	0.8	0.1	0.8	1.7	2.0	0.9

SUBSTITUTE SHEET (RULE 26)

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E. Basophil and eosinophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Batf5/SI	
21157_s_at	M36651_1 M73914_1	R	0.6 0.2	1.8 1.6	282 153	164 187	253 402	297 33.0	295 0.3	0.0 0.7	0.0 1.5	0.0 0.1	0.0 0.1	0.0 0.1	0.0 0.1	0.0 0.1	0.0 0.1	0.0 0.1	0.0 0.1	0.0 0.1	61956 42811		
21074_s_at	M73914_1	R	0.7 0.2	1.8 1.6	282 153	164 187	253 402	297 33.0	295 0.3	0.0 0.7	0.0 1.5	0.0 0.1	0.0 0.1	0.0 0.1	0.0 0.1	0.0 0.1	0.0 0.1	0.0 0.1	0.0 0.1	0.0 0.1	0.0 0.1		
206361_at	NM_004778_1	GPR	1.8 1.7 0.2	0.3 2.0 0.1	405 2191 435	153 2036 330	337 2268 4.1	379 233.8 88	423 163.1 233	1.0 2.1 0.1	2.6 1.94 0.1	2.2 1.91 0.1	2.1 1.93 0.3	0.8 0.28 0.1	1.4 1.4 0.1	1.0 1.2 0.1	0.9 0.9 0.1	0.7 0.7 0.1	0.5 0.7 0.1	0.5 0.7 0.1	16642 15164 13357		
206207_at	NM_001883_1	GPR	1.8 1.7 0.2	0.3 2.0 0.1	405 2191 435	153 2036 330	337 2268 4.1	379 233.8 88	423 163.1 233	1.0 2.1 0.1	2.6 1.94 0.1	2.2 1.91 0.1	2.1 1.93 0.3	0.8 0.28 0.1	1.4 1.4 0.1	1.0 1.2 0.1	0.9 0.9 0.1	0.7 0.7 0.1	0.5 0.7 0.1	16642 15164 13357			
203638_s_at	NM_022369_1	R	0.7 0.2	1.8 1.6	282 153	164 187	253 402	297 33.0	295 0.3	0.0 0.7	0.0 1.5	0.0 0.1	0.0 0.1	0.0 0.1	0.0 0.1	0.0 0.1	0.0 0.1	0.0 0.1	0.0 0.1	0.0 0.1			
207111_at	NM_001974_1	GPR	1.5 0.7	0.1 0.3	495 5.7	345 52	85.9 45	93.1 2.1	91.2 2.8	2.7 1.0	3.7 1.0	3.7 1.0	3.7 1.0	5.1 0.1	3.4 0.1	1.7 0.1	0.8 0.1	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1		
215248_at	AT50033	GPR	0.1 0.2	0.6 0.5	5.1 4.5	4.1 12.5	83 26	90 42	154 29	1.3 0.6	0.9 1.1	0.9 1.1	0.9 1.1	0.9 0.4	0.3 0.4	0.4 0.4	0.4 0.4	0.4 0.4	0.4 0.4	0.4 0.4	0.4 0.4		
205471_s_at	AW77082	GPR	0.1 0.2	0.6 0.5	5.1 4.5	353 101.5	186 760	137 26.8	163 34.1	1.7 40.5	0.9 3.6	1.7 4.5	1.7 6.3	1.7 4.5	0.9 0.4	0.3 0.5	0.4 0.5	0.4 0.5	0.4 0.5	0.4 0.5	0.4 0.5		
218837_s_at	NM_025090_1	GPR	0.1 0.2	0.6 0.5	5.1 4.5	353 101.5	186 760	137 26.8	163 34.1	1.7 40.5	0.9 3.6	1.7 4.5	1.7 6.3	1.7 4.5	0.9 0.4	0.3 0.5	0.4 0.5	0.4 0.5	0.4 0.5	0.4 0.5	0.4 0.5		
201769_s_at	NM_02164_1	GPR	0.1 0.2	0.6 0.5	5.1 4.5	353 101.5	186 760	137 26.8	163 34.1	1.7 40.5	0.9 3.6	1.7 4.5	1.7 6.3	1.7 4.5	0.9 0.4	0.3 0.5	0.4 0.5	0.4 0.5	0.4 0.5	0.4 0.5	0.4 0.5		
208828_s_at	M87771_1	GPR	0.3 0.8	1.4 0.9	3.7 10.8	102 6.0	83 20.6	39 6.7	89 6.1	4.5 25.8	83 20.6	0.8 1.3	1.4 1.4	1.4 1.4	1.4 1.4	1.1 4.5	1.3 4.2	0.7 2.9	0.7 2.1	0.7 3.7	0.5 0.5	1.1 1.1	
213650_s_at	AL049887_1	GPR	0.3 0.8	1.4 0.9	3.7 10.8	102 6.0	83 20.6	39 6.7	89 6.1	4.5 25.8	83 20.6	0.8 1.3	1.4 1.4	1.4 1.4	1.4 1.4	1.1 4.5	1.3 4.2	0.7 2.9	0.7 2.1	0.7 3.7	0.5 0.5	1.1 1.1	
2059382_s_at	AL057637	GPR	0.3 0.8	1.4 0.9	3.7 10.8	102 6.0	83 20.6	39 6.7	89 6.1	4.5 25.8	83 20.6	0.8 1.3	1.4 1.4	1.4 1.4	1.4 1.4	1.1 4.5	1.3 4.2	0.7 2.9	0.7 2.1	0.7 3.7	0.5 0.5	1.1 1.1	
22007_at	NM_016382_1	R	0.5 0.2	0.1 0.2	15.7 5.2	87.0 7.7	65.4 6.9	99 5.9	108 10.2	26.6 12.7	18.5 11.1	0.3 0.2	0.4 0.3	1.2 1.1	3.0 3.0	0.1 0.1	0.4 0.4	3.5 3.5	5.2 5.2	1.1 1.1	0.1 0.1	4.6297	
210108_at	BE55399	[CN]	0.2 0.2	0.1 0.1	1.0 1.7	24 1.0	0.8 1.7	2.4 2.4	0.8 0.8	2.4 2.4	18 18.0	0.6 0.6	0.5 0.5	0.5 0.5	0.0 0.0	0.3 0.3	0.1 0.1	0.0 0.0	0.3 0.3	0.0 0.0	0.3 0.3	4.5958	
209193_at	M24779_1	GPR	0.8 0.2	7.1 6.3	110.3 100.1	100.1 47.0	79.7 79.7	91.6 91.6	79.5 192	18.8 18.8	21.1 21.1	16.1 16.1	4.1 4.1	12.7 13.9	13.9 4.6	4.0 4.0	12 12	4.1983	4.1983	4.1983	4.1983		
202794_at	NM_002194_2	GPR	5.7 0.2	6.2 1.1	7.1 107.2	25.8 142.9	20.5 102.4	17.9 46.4	53.6 91.7	57.8 118.1	2.7 107.5	2.7 28.3	2.7 200	2.7 26.3	2.7 25.1	0.2 0.2	0.5 0.5	0.4 0.4	0.2 0.2	0.4 0.4	0.4 0.4	4.1158	
208304_at	NM_001837_1	GPR	0.2 0.2	0.6 0.5	5.1 33.7	71.4 7.1	38.4 43	104.7 5.1	80.8 8.0	47.7 8.0	45.1 6.4	20 10	23 0.8	3.1 0.7	2.8 0.7	1.4 1.4	0.7 0.7	0.4 0.4	0.2 0.2	0.4 0.4	0.4 0.4	3.9525	
206111_at	NM_002934_1	GPR	0.2 0.2	0.6 0.5	5.1 33.7	71.4 7.1	38.4 43	104.7 5.1	80.8 8.0	47.7 8.0	45.1 6.4	20 10	23 0.8	3.1 0.7	2.8 0.7	1.4 1.4	0.7 0.7	0.4 0.4	0.2 0.2	0.4 0.4	0.4 0.4	3.7641	
4327_at	AI9788	GPR	0.8 0.2	0.7 2.1	4.3 48	5.1 4.8	43 4.8	5.1 4.8	8.0 8.0	8.0 8.0	8.0 8.0	8.0 8.0	8.0 8.0	8.0 8.0	8.0 8.0	1.0 1.0	1.0 1.0	1.0 1.0	1.0 1.0	1.0 1.0	1.0 1.0	3.7554	
218904_at	AI03984	GPR	0.6 0.2	1.2 1.1	4.3 44.1	56.2 72.3	56.2 50.5	56.2 18.8	56.6 38.8	63 70.3	9.7 29.9	0.7 1.2	0.5 1.2	0.5 1.2	0.5 1.2	2.2 1.8	1.7 1.8	1.4 1.6	1.2 1.6	1.4 1.5	1.0 1.5	1.9 3.0	1.3 0.6
208906_at	U62027_1	GPR	0.6 0.2	1.2 1.1	4.3 44.1	56.2 72.3	56.2 50.5	56.2 18.8	56.6 38.8	63 70.3	9.7 29.9	0.7 1.2	0.5 1.2	0.5 1.2	0.5 1.2	2.2 1.8	1.7 1.8	1.4 1.6	1.2 1.6	1.4 1.5	1.0 1.5	1.9 3.0	1.3 0.6
207894_at	A1539710	GPR	0.6 0.2	1.2 1.1	4.3 44.1	56.2 72.3	56.2 50.5	56.2 18.8	56.6 38.8	63 70.3	9.7 29.9	0.7 1.2	0.5 1.2	0.5 1.2	0.5 1.2	2.2 1.8	1.7 1.8	1.4 1.6	1.2 1.6	1.4 1.5	1.0 1.5	1.9 3.0	1.3 0.6
221675_s_at	AF195624_1	GPR	0.6 0.2	1.2 1.1	4.3 44.1	56.2 72.3	56.2 50.5	56.2 18.8	56.6 38.8	63 70.3	9.7 29.9	0.7 1.2	0.5 1.2	0.5 1.2	0.5 1.2	2.2 1.8	1.7 1.8	1.4 1.6	1.2 1.6	1.4 1.5	1.0 1.5	1.9 3.0	1.3 0.6
202562_s_at	BL003629_1	GPR	0.6 0.2	1.2 1.1	4.3 44.1	56.2 72.3	56.2 50.5	56.2 18.8	56.6 38.8	63 70.3	9.7 29.9	0.7 1.2	0.5 1.2	0.5 1.2	0.5 1.2	2.2 1.8	1.7 1.8	1.4 1.6	1.2 1.6	1.4 1.5	1.0 1.5	1.9 3.0	1.3 0.6
219919_s_at	NM_018276_1	GPR	0.6 0.2	1.2 1.1	4.3 44.1	56.2 72.3	56.2 50.5	56.2 18.8	56.6 38.8	63 70.3	9.7 29.9	0.7 1.2	0.5 1.2	0.5 1.2	0.5 1.2	2.2 1.8	1.7 1.8	1.4 1.6	1.2 1.6	1.4 1.5	1.0 1.5	1.9 3.0	1.3 0.6
204301_at	NM_014867_1	GPR	0.6 0.2	1.2 1.1	4.3 44.1	56.2 72.3	56.2 50.5	56.2 18.8	56.6 38.8	63 70.3	9.7 29.9	0.7 1.2	0.5 1.2	0.5 1.2	0.5 1.2	2.2 1.8	1.7 1.8	1.4 1.6	1.2 1.6	1.4 1.5	1.0 1.5	1.9 3.0	1.3 0.6
210999_s_at	U66065_1	GPR	3.6 1.7	1.7 8.4	13.6 13.6	118 118	73 73	4.6 4.6	48 48	64 64	22 22	1.7 1.7	1.9 1.9	1.9 1.9	1.9 1.9	1.2 1.2	1.2 1.2	1.2 1.2	1.2 1.2	1.2 1.2	1.2 1.2	1.6 1.6	
209539_at	D25304_1	Guanine exchange factor	13.1 19.2	24.8 11.4	288 202	74.7 67.0	73.0 67.0	53.8 37.4	355 42.4	92.9 85.4	92.1 69.8	185 17.6	137 21.5	31 26	129 12.6	71 8.4	78 8.4	10.2 12.7	10.2 12.7	10.2 12.7	10.2 12.7	10.2 12.7	
208921_s_at	L12387_1	Ser/Thr kinase	19.9 19.2	16.1 11.4	390 202	87.1 88.6	75.2 67.0	66.4 37.4	68.7 42.4	89.4 86.3	71.4 17.6	138 12.6	20.0 10.2	46.5 4.6	89.6 8.4	67 6.1	4.4 0.1	10.6 0.1	11.0 0.1	11.0 0.1	11.0 0.1	11.0 0.1	
209043_at	A5033026_1	5'-phosphosulfate kinase	19.9 19.2	16.1 11.4	390 202	87.1 88.6	75.2 67.0	66.4 37.4	68.7 42.4	89.4 86.3	71.4 17.6	138 12.6	20.0 10.2	46.5 4.6	89.6 8.4	67 6.1	4.4 0.1	10.6 0.1	11.0 0.1	11.0 0.1	11.0 0.1	11.0 0.1	

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E. Eosinophil and neutrophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC, cord blood	MC, lung	Ba 2 (small) 1	Ba 3 (small) 1	Eo (small) 1	Eo 3 (small) 1	Eo 4 (small) 1	Ne (small) 1	Ne 3 (small) 1	Ne 4 (small) 1	Pl	CD4	CD8	CD14	CD19	Fb	Eo/Ne S.I.
221345_at	NM_005306.1	GPR GPR43/PAR1-like zinc finger, D-H-H-C domain containing 18	0.1 0.4	0.9 0.6	0.6 0.7	16.6 15.4	10.5 49.7	45.7 225	23.0 225	0.8 0.7	0.1 0.7	0.1 0.7	0.4 0.7	21.742					
212860_at	BC168720	solute carrier family 19 member 1 nephroblastoma overexpressed gene 1 ARF-GAP, RHO-GAP, ankyrin repeat and plectin homology domains-containing protein 3	2.2 0.8	4.1 3.9	4.0 16.0	17.4 14.8	16.7 59.2	53.9 30.9	39.8 1.1	2.4 2.8	2.6 1.5	1.3 1.3	65.942						
211576_s_at	BC03068.1		1.4 0.1	0.7 1.4	0.7 5.1	5.9 11.5	12.4 19.8	18.7 27.1	28.1 1.8	0.9 0.4	2.7 0.5	0.8 0.8	4.99						
214321_at	BF440025		1.3 1.0	0.8 0.2	0.7 62	72 17.0	13.7 45	7.6 10.7	11.3 0.1	0.1 0.1	0.1 0.1	0.1 0.1	4.9823						
218950_at	NM_022481.1		1.4 3.1	24 3.7	2.1 15.5	15.9 18.3	15.5 28.0	24.3 15.9	20.6 0.7	0.2 0.8	3.9 3.9	0.9 1.0	4.829						
205681_at	NM_004049.1	BCL2-related protein A1 grancalcin cDNA FLJ36416/fis, clone	0.5 1.9	1.0 3.2	2.4 52.4	40.2 35.9	30.5 46.5	49.2 35.5	33.5 1.5	2.2 1.9	8.3 8.3	4.3 4.3	0.2 0.2	4.7782					
203755_at	NM_012198.1	THYMU2011053 hypothetical protein PRD0831 homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2 KIAA0599	5.0 2.4	1.6 1.0	1.0 33.2	37.1 68.7	40.6 63.2	77.8 89.2	80.9 3.0	3.0 2.8	13.5 13.5	4.1 4.1	7.8 7.8	4.2603					
213241_at	AF055307.1		1.2 1.4	1.3 0.5	1.6 10.1	8.8 11.2	6.4 5.0	6.2 4.0	3.8 1.6	0.8 0.2	1.4 1.4	0.9 0.6	4.1325						
221815_at	BE671816		0.1 0.6	1.0 1.2	3.1 9.1	10.4 18.2	16.6 9.7	9.7 14.5	15.2 0.8	0.9 1.2	0.7 0.7	2.3 2.3	0.1 0.1	4.0797					
214153_at	BE467941	Edge4, endothelial differentiation lysophosphatidic acid	0.1 0.1	0.4 1.2	0.9 4.6	2.8 4.7	3.4 4.4	3.5 6.0	7.9 0.4	0.2 0.4	0.3 0.3	0.0 0.0	3.727						
212821_at	AU147160		1.2 1.4	2.1 3.6	2.6 13.7	8.0 19.6	22.3 24.6	17.0 26.1	29.1 0.1	3.6 5.0	3.8 3.8	1.9 1.9	0.9 0.9	3.7119					
206723_s_at	AF011466.1	GPR G-protein-coupled receptor 4 adenosine monophosphate deaminase 2 [isoform_1] transforming, acidic coiled-coil containing protein 3 (TAC3) protein kinase C-like 2 serum/glucocorticoid regulated kinase (SGK)	1.0 2.0	2.6 5.9	4.6 26.6	18.7 30.2	31.9 78.7	63.1 79.5	91.3 3.4	5.8 6.1	12.6 12.6	3.7 3.7	5.8 5.8	3.5888					
212300_at	A1916249		0.4 0.4	4.8 8.3	95 33	24 33	4.7 17.6	14.8 23.5	22.8 2.4	2.3 2.3	3.6 3.6	1.0 1.0	0.7 0.7	3.4769					
218308_at	NM_006342.1		1.9 0.6	3.1 3.7	5.1 11.8	7.6 17.7	13.8 16.7	23.6 27.0	28.4 1.1	2.1 2.2	4.2 4.2	2.9 2.9	3.2963						
212629_s_at	AK023692.1		30.2 25.2	1.9 18.5	25.4 114.1	116.0 150.9	164.8 60.2	77.1 105.8	156.3 1.1	3.7 3.7	34.6 34.6	16.189							
201739_at	NM_005627.1	ectonucleotide triphosphate diphosphohydrolase 1 growth arrest and DNA damage inducible protein beta (GADD45B)	1.4 0.6	2.1 1.6	2.0 15.9	22.3 39.5	29.1 14.1	13.7 23.7	13.8 2.6	2.6 1.3	6.5 6.5	4.8 4.8	0.6 0.6	3.0752					
209473_at	AV717590		2.0 0.3	2.7 4.5	3.6 15.5	11.9 16.3	34.4 7.0	12.0 13.5	9.4 0.4	3.1 3.1	4.2 4.2	1.1 1.1	0.6 0.6	3.0295					
209304_x_at	AF087853.1		0.1 0.3	1.3 0.5	1.7 7.1	2.9 3.3	3.8 6.1	5.1 5.2	10.8 0.4	0.1 0.1	0.9 0.9	0.7 0.7	0.4 0.4	3.0005					
210666_at	AF050145.1		32/36																

SUBSTITUTE SHEET (RULE 26)**Fig. 6N**

G. Basophil and neutrophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC.												Ne4 (small) (small)	Ne3 (small) (small)	Ne4 1 2	Eo4 1 2	Eo3 1 2	Eo 1 2	Ba3 1 2	Ba2 1 2	Ba1 1 2	MC. blood lung	cord
			Ba1	Ba2	Ba3	Ba4	CD8	CD14	CD19	Fb	Ba+Ne.SL														
218739_at	NM_016006.1	CG158 protein	1.8	1.8	1.7	1.7	16.3	17.3	2.6	3.3	3.2	25	20.7	23.6	21.4	19.3	13	12	0.7	29	0.7	15	5.81398		
21922_at	NM_025180.1	FLJ3386	1.0	0.3	10.1	23.5	18.8	24	3.7	4.5	42	13.7	14.0	26.1	27.7	0.1	0.5	1.6	1.0	0.6	25	4.97025			
219157_at	NM_007246.1	kelch (Drosophila)-like2	2.4	1.7	4.2	16.2	19.2	3.6	2.5	4.3	3.8	15.5	24.4	24.5	22.5	0.7	2.0	1.5	3.0	22	1.7	4.61523			
206633_at	NM_0021082	histidine ammonia-lyase	0.1	1.4	8.5	13.7	25.4	0.2	0.6	1.3	0.6	31.4	32.8	61.7	37.0	1.6	0.5	0.1	5.6	0.6	0.5	4.57355			
213935_at	AF007132.1	clone 23551 mRNA	0.8	0.1	5.0	26.2	26.4	2.4	1.7	2.9	12	4.5	6.7	11.2	9.0	0.1	0.1	0.2	2.3	0.5	0.8	4.33664			
222151_s_at	AK02378.1	FLJ3676 ffs	1.0	0.9	4.5	5.5	4.7	1.8	1.7	1.4	1.6	8.4	10.2	8.4	7.6	0.5	0.8	1.3	0.8	1.0	1.3	4.14372			
207907_at	NM_003807.1	tumor necrosis factor (ligand) superfamily member 14 (TNFSF14)	0.1	0.1	3.9	10.4	6.3	1.2	1.5	4.0	4.1	15.8	7.3	15.8	11.5	0.2	0.4	0.1	0.6	0.0	0.1	3.89177			
202530_at	NM_001315.1	mitogen-activated protein kinase 14	5.0	3.0	28.8	82.2	70.8	4.0	7.1	13.9	11.1	13.6	23.0	25.7	22.3	5.3	29	35	73	26	45	3.84469			
217521_at	N54942	Hs276590 ESTs	0.1	0.1	5.5	18.9	20.9	0.3	0.3	1.6	0.1	19.6	14.5	29.9	18.4	0.4	0.8	0.9	4.3	1.0	0.3	3.84207			
203653_s_at	NM_0019492	E2F transcription factor 3	2.5	1.7	4.3	16.2	13.2	2.1	1.9	5.7	3.3	8.8	11.7	13.3	15.4	1.5	1.4	2.5	2.3	1.1	1.2	3.7116			
203420_at	NM_016255.1	autosomal highly conserved protein (AHCP)	2.4	3.3	15.6	31.5	32.4	7.3	6.6	14.3	11.0	37.2	37.2	48.5	50.0	6.1	5.0	9.8	4.5	3.3	9.8	3.48188			
218308_at	NM_006342.1	transforming acidic coiled-coil containing protein 3	0.4	0.4	4.8	8.3	9.5	3.3	2.4	3.3	4.7	17.6	14.8	23.5	22.8	2.4	2.3	1.6	3.6	1.0	0.7	3.4769			
203080_s_at	NM_013450.1	bromodomain adjacent to zinc finger domain 2B	2.2	2.4	10.4	22.8	22.9	4.9	6.6	10.0	9.5	29.5	30.7	33.5	40.6	1.1	1.7	1.9	4.6	2.3	1.5	3.401			
219999_at	NM_018621.1	hypothetical protein PRO2198	0.4	0.6	3.9	7.6	8.0	20	1.5	3.9	2.7	9.8	6.5	11.7	12.3	0.2	1.3	1.8	2.4	1.7	0.9	3.31991			
213805_at	A1692428	clone 23551 mRNA	0.3	0.1	13.8	11.0	8.7	3.2	3.0	1.4	1.4	19.7	16.7	5.3	7.0	0.7	0.2	0.8	3.3	0.4	0.7	3.29317			
204689_s_at	NM_0072192	ring finger protein 24	0.9	0.2	4.4	27.9	34.3	2.1	5.9	16.1	14.5	18.8	14.4	60.7	56.1	0.5	0.1	0.1	0.1	0.1	0.8	3.18834			
215555_at	AK023774.1	FLJ3772 ffs	0.0	0.4	5.0	4.3	5.8	15	1.9	1.5	1.5	7.6	8.2	3.3	32	0.9	1.0	1.5	1.5	1.0	0.1	3.1591			

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Fig. 6O

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H. Mast cell and basophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC, cord	MC, blood	Ba 1 (small)	Ba 2 (small)	Eo	Eo 3 (small)	Eo 4 (small)	Ne 3 (small)	Ne 4 (small)	pI	CD4	CD8	CD14	CD19	Fb	MC+Ba SJ.	
205624_at	NM_001870.1	carboxypeptidase A3	137.1	91.0	107.6	139.0	173.1	25	1.6	2.8	1.9	0.1	1.4	2.0	124.0	0.2	0.2	0.5	
208605_s_at	NM_0025292	R	8.0	12	4.6	9.3	8.1	0.2	0.0	0.1	0.2	0.0	0.1	0.7	0.1	0.1	0.0	0.0	
210258_at	AF030107.1	TRK neurotrophin receptor regulator of G protein signaling (RG513)	6.2	8.4	5.6	7.1	10.9	0.3	0.4	0.5	0.5	0.0	0.1	0.3	0.1	0.0	0.2	34.7309	
207496_at	NM_000139.1	R	19.9	24.7	35.4	51.9	45.6	0.9	0.1	0.5	0.3	0.1	0.1	1.8	1.6	0.5	0.2	59.1989	
205837_at	AI269290	solute carrier family 18	24.3	27.1	8.1	22.3	25.0	1.3	1.0	0.8	0.9	1.3	0.9	0.5	0.7	0.9	0.4	0.0	
210358_X_at	BC002557.1	GATA-binding protein 2	18.4	12.8	55.0	31.7	24.7	2.0	1.6	1.9	1.7	0.9	1.9	1.3	3.7	2.6	0.8	0.9	
207497_s_at	D10583.1	F epsilon R beta	10.7	28.6	34.9	12.6	6.8	15	1.0	0.8	0.8	1.9	0.9	1.7	1.5	1.7	0.7	0.3	
203914_X_at	NM_000860.1	15-hydroxyprostaglandin dehydrogenase (PDGH)	63.9	51.4	24.8	36.0	23.3	4.1	4.6	4.6	2.6	1.3	0.9	1.3	1.2	6.0	1.4	1.5	6.14285
219557_s_at	NM_020645.1	chromosome 11 open reading frame 14	7.4	42	4.4	7.4	6.6	12	1.6	2.0	24	0.9	1.9	1.1	2.1	1.1	1.4	1.5	3.38029
204061_at	NM_005044.1	protein kinase X-linked	6.2	52	52	12.8	16.9	23	2.7	2.5	2.4	0.8	0.4	0.7	1.2	1.9	1.5	2.5	3.26862
202068_s_at	NM_000527.2	R	24.6	16.8	19.3	28.5	135	1.6	1.0	1.6	0.9	0.8	2.4	1.5	2.5	2.3	3.4	0.8	
																		3.1679	

Fig. 6P

Fig. 6Q

I. Specific transcripts markers for non-granulocytes.

J. Raw AD levels for the median values used to normalize the raw AD levels, and the housekeeping genes.

Probe set	Accession #	Transcripts	MC cord	MC blood	Ba 2 (small)	Ba 1 (small)	Eo 2	Eo 1	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)
AFFX-HSAC07/X00351_3_at	X00351	beta-actin	18334	19383	14638	20322	19151	2019	18638	21153	18588	19406	22202	16589
AFFX-HSAC07/X00351_M_at	X00351	beta-actin	22898	21777	12940	11533	7608	22560	18785	14861	13431	23106	23373	6861
AFFX-HSAC07/X00351_5_at	X00351	beta-actin	15642	15838	9516	2927	2066	17186	21061	4861	3771	18772	19768	2165
AFFX-HUMGAPDH/M33197_3_at	M33197	GAPDH	14906	13632	3640	10477	9332	2649	2844	5498	2605	2549	3186	3586
AFFX-HUMGAPDH/M33197_N_at	M33197	GAPDH	15891	16852	3218	7587	6963	2382	2565	3720	1838	2194	2796	2312
AFFX-HUMGAPDH/M33197_5_at	M33197	GAPDH	16298	16701	3479	4559	5110	1827	3121	2127	1168	2492	3476	1636
The median value of 22283 transcripts			121	1693	853	1122	1109	93.7	102.1	127.3	114	62.7	73.1	87.4

Abbreviations used in the table A-1 were (small); the results obtained by the small sample protocol (see materials and methods), R; receptor, and IC₅₀; ion channel.

Fig. 6R